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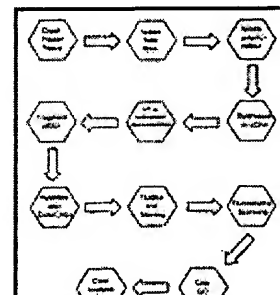
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**(54) Title:** GENE EXPRESSION PROFILES IN LIVER CANCER

**(57) Abstract**

The present invention identifies the global changes in gene expression associated with liver cancer by examining gene expression in tissue from normal liver, metastatic malignant liver and hepatocellular carcinoma. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.



## Description Claims

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**GENE EXPRESSION PROFILES IN LIVER CANCER RELATED APPLICATIONS** This application is related to U. S. Provisional Application 60/211,379, filed on June 14,2000, and is related to U. S. Provisional Application 60/237,054, filed October 2,2000, and is related to U. S. Application 09/880,107, filed June 14,2001, each of which is herein incorporated by reference in its entirety.

**BACKGROUND OF THE INVENTION** Primary hepatocellular carcinoma (HCC) is a widespread cancer throughout the world, especially prevalent where the incidence of chronic hepatitis B (HBV) and hepatitis C (HCV) viral infections are endemic (Groen, (1999) *Semin. Oncol. Nurs.* 15,48-57; Idilman et al., (1998) *J. Viral. Hepat.* 5,110-117; Di Bisceglie et al., (1998) *Hepatol.* 28, 1161-1165; Johnson, (1997) *Hepatogastroenterology*44, 307-312; Sheu, (1997) *J.*

*Gastroenterol. Hepatol.* 12, S309-313). Hepatocellular carcinomas are very malignant tumors that generally offer a poor prognosis, dependent on the size of the tumor, the effect on normal liver functions, and the involvement of metastases. They are best treated by surgical resection, when the tumors are diagnosed at a stage where this is a viable possibility, but the recurrence rate for these cancers remains high (Johnson, (1997) *Hepatogastroenterology* 44, 307-312; Schafer & Sorrel, (1999) *Lancet* 353,1253-1257; Groen, (1999) *Semin. Oncol. Nurs.* 15,48-57; Sitzman, (1995) *World. J. Surg.* 19,790-794; DiCarlo, (1995) *Hepato-Gastroenterol.* 42,222-259; Tanaka et al., (1996) *Hepato-Gastroenterol.* 43,1172-1181; El-Assal et al., (1997) *Surgery* 122,571-577).

Numerous risk factors for the development of HCC have been identified: cirrhosis, HBV or HCV infection, being male, alcohol-related liver disease, exposure to aflatoxins, vinyl chloride and radioactive thorium dioxide, cigarette smoking, ingestion of inorganic arsenic, the use of oral contraceptives and anabolic steroids, iron accumulation, and various inherited metabolic disorders (hemochromatosis, glycogen storage disease, porphyria, tyrosinemia, oc-l-antitrypsin deficiency) (Di Bisceglie et al., (1998) *Hepatol.* 28,1161-1165; Chen et al., (1997) *J. Gastroenterol. Hepatol.* 12, S294-308 ; Schafer & Sorrell (1999) *Lancet* 353,1253-1257; Groen, (1999) *Semin. Oncol. Nurs.* 15,48-57; Idilman et al., (1998) *J. Viral. Hepat.* 5,110-117; Johnson, (1997) *Hepato-Gastroenterol.* 44,307-312).

In addition to liver tumors attributed to hepatocellular carcinoma, there are liver tumors that arise as metastases from primary tumors in other parts of the body. These tumors most often metastasize from the gastrointestinal organs, primarily the colon and rectum, but it is possible for metastatic liver cancers to occur from primary cancers throughout the body (Sitzman, (1990) *Hepatic Neoplasia*, in Bayless (editor) *Current Therapy in Gastroenterology and Liver Disease*, Marcel Dekker; Groen, (1999) *Semin.*

*Oncol. Nurs.* 15,48-57). These cancers can be treated using the routine therapies such as chemotherapy, radiotherapy, surgical resection, liver transplantation, chemoembolization, cryosurgery, or a combination of therapies (Sitzman 1990, Groen 1999).

The characterization of genes that are differentially expressed in tumorigenesis is an important step in identifying those that are intimately involved in the details of a cell's transformation from normal to cancerous. Little is known about the molecular changes that take place in the liver during the course of tumor progression. While changes in the expression level of individual genes has been reported, for example, galectin-3 (Hsu et al., (1999) *Int. J. Cancer* 81: 519-526; Iurisci et al., (2000) *Clin. Cancer Res.* 6: 1389-1393; Nakamura et al., (1999) *Int. J. Oncol.* 15: 143-148) and pancreatic secretory trypsin inhibitor (PTSI, Ohmachi et al., (1994) *Int. J. Cancer* 55: 728-734) the investigation of the global changes in gene expression which occur in liver have not been documented. The identification of genes that are expressed in tumor tissue at differing levels, but not expressed at any level in normal liver tissue

will be very valuable for monitoring tumor progression. The identification of genes and ESTs that are expressed in both types of tumors, i. e., primary hepatocellular carcinomas as well as metastatic tumors of a different origin, and not in normal liver cells would be extremely valuable for the diagnosis of liver cancer. Thus there exists a need in the art for the identification of new genes and ESTs to serve as molecular markers to monitor the onset and development of liver cancer. These and other needs are met by the present invention.

**SUMMARY OF THE INVENTION** The present invention identifies the global changes in gene expression associated with liver cancer by examining gene expression in tissue from normal liver, metastatic malignant liver and hepatocellular carcinoma. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

The invention includes methods of diagnosing the presence or absence of liver cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5. In some preferred embodiments, the method may include detecting the expression level of one or more genes selected from a group consisting Tetraspan NET-6 protein; collagen, type V, alpha; and glypican 3.

The invention also includes methods of detecting the progression of liver cancer and/or differentiating nonmetastatic from metastatic disease. For instance, methods of the invention include detecting the progression of liver cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer progression. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In some aspects, the present invention provides a method of monitoring the treatment of a patient with liver cancer, comprising administering a pharmaceutical composition to the patient and preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising liver cancer cells or to both. In some preferred embodiments, the gene profile will include the expression level of one or more genes in Tables 3-9. In other preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In another aspect, the present invention provides a method of treating a patient with liver cancer, comprising administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising liver cancer cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In one aspect, the present invention provides a method of diagnosing hepatocellular carcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

In another aspect, the present invention provides a method of detecting the progression of hepatocellular carcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma progression.

In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

The present invention also provides materials and methods for monitoring the treatment of a patient with a hepatocellular carcinoma. The present invention provides a method of monitoring the treatment of a patient with hepatocellular carcinoma, comprising administering a pharmaceutical composition to the patient, preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising hepatocellular carcinoma cells or to both. In some preferred embodiments, the method may include detecting the level of expression of one or more genes from the genes listed in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

In a related aspect, the present invention provides a method of treating a patient with hepatocellular carcinoma, comprising administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3- 9, preparing a gene expression profile from a cell or tissue sample from the patient comprising hepatocellular carcinoma cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising hepatocellular carcinoma cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

The present invention provides a method of diagnosing a metastatic liver tumor in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver tumor. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

The present invention provides a method of detecting the progression of a metastatic liver tumor in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver tumor progression. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

In a related aspect, the present invention provides a method of monitoring the treatment of a patient with a metastatic liver tumor, comprising administering a pharmaceutical composition to the patient, preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising metastatic liver tumor cells or to both. In some preferred embodiments, the method of the present invention may include detecting the expression level of one or more genes selected from the genes listed in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

In some preferred embodiments, the present invention provides a method of treating a patient with a metastatic liver tumor, comprising administering to the patient a pharmaceutical composition, wherein



the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising metastatic liver tumor cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising metastatic liver tumor cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

The invention also includes methods of differentiating metastatic liver cancer from hepatocellular carcinoma in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer rather than hepatocellular carcinoma.

The invention further includes methods of screening for an agent capable of modulating the onset or progression of liver cancer, comprising the steps of exposing a cell to the agent; and detecting the expression level of two or more genes from Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

Any of the methods of the invention described above may include the detection of at least 2 genes from the tables. Preferred methods may detect all or nearly all of the genes in the tables. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

The invention further includes compositions comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9 as well as solid supports comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

The invention further includes computer systems comprising a database containing information identifying the expression level in liver tissue of a set of genes comprising at least two genes in Tables 3-9; and a user interface to view the information. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5. The database may further include sequence information for the genes, information identifying the expression level for the set of genes in normal liver tissue and malignant tissue (metastatic and nonmetastatic) and may contain links to external databases such as GenBank.

Lastly, the invention includes methods of using the databases, such as methods of using the disclosed computer systems to present information identifying the expression level in a tissue or cell of at least one gene in Tables 3-9, comprising the step of comparing the expression level of at least one gene in Tables 3-9 in the tissue or cell to the level of expression of the gene in the database. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

**BRIEF DESCRIPTION OF THE DRAWINGS** Figure 1 is a flow chart showing a schematic representation of the experimental protocol.

Figures 2A-2C are graphs of the number of genes present in all samples as a function of the number of samples for the second sample set.

**DETAILED DESCRIPTION** Many biological functions are accomplished by altering the expression of various genes through transcriptional (e. g., through control of initiation, provision of RNA precursors,

RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death, are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression also are associated with pathogenesis. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes could lead to tumorigenesis or hyperplastic growth of cells (Marshall, (1991) *Cell*, 64,313-326; Weinberg, (1991) *Science*, 254,1138-1146).

Thus, changes in the expression levels of particular genes (e. g., oncogenes or tumor suppressors) serve as signposts for the presence and progression of various diseases.

Monitoring changes in gene expression may also provide certain advantages during drug screening development. Often drugs are screened and prescreened for the ability to interact with a major target without regard to other effects the drugs have on cells. Often such other effects cause toxicity in the whole animal, which prevent the development and use of the potential drug.

The present inventors have examined tissue samples from normal liver, metastatic malignant liver and hepatocellular carcinoma to identify the global changes in gene expression associated with liver cancer. The protocol used is schematically represented in Figure 1. These global changes in gene expression, also referred to as expression profiles, provide useful markers for diagnostic uses as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Definitions In the description that follows, numerous terms and phrases known to those skilled in the art are used. In the interests of clarity and consistency of interpretation, the definitions of certain terms and phrases are provided.

The present invention provides compositions and methods to detect the level of expression of genes that may be differentially expressed dependent upon the state of the cell, i. e., normal versus cancerous. As used herein, the phrase "detecting the level of expression" includes methods that quantitate expression levels as well as methods that determine whether a gene of interest is expressed at all. Thus, an assay which provides a yes or no result without necessarily providing quantification of an amount of expression is an assay that requires "detecting the level of expression" as that phrase is used herein.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described herein, refers to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequence of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

"Bind (s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (e. g., the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may

be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation.

Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (e. g., probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids).

Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

The phrase "hybridizing specifically to" refers to the binding, duplexing or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (e. g., total cellular) DNA or RNA.

The term "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence.

For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

While the mismatch (s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe." As used herein a "probe" is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i. e., A, G, U, C or T) or modified bases (7- deazaguanosine, inosine, etc.). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T<sub>m</sub>) for the

specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e. g., 10 to 50 nucleotide). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (i. e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical monomer unit (e. g., nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Homology or identity may be determined by BLAST (Basic Local Alignment Search Tool) analysis using the algorithm employed by the programs blastp, blastn, blastx, tblastn and tblastx (Karin et al., (1990) Proc. Natl. Acad. Sci. USA 87,2264-2268 and Altschul, (1993) J. Mol. Evol. 36,290-300, fully incorporated by reference) which are tailored for sequence similarity searching. The approach used by the BLAST program is to first consider similar segments between a query sequence and a database sequence, then to evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases, see Altschul et al., (1994) Nature Genet. 6,119-129) which is fully incorporated by reference. The search parameters for histogram, descriptions, alignments, expect (i. e., the statistical significance threshold for reporting matches against database sequences), cutoff, matrix and filter are at the default settings. The default scoring matrix used by blastp, blastx, tblastn, and tblastx is the BLOSUM62 matrix (Henikoff et al., (1992) Proc. Natl. Acad. Sci. USA 89, 10915- 10919, fully incorporated by reference). Four blastn parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at everywinkth position along the query); and gapw=16 (sets the window width within which gapped alignments are generated). The equivalent Blastp parameter settings were Q=9; R=2; wink=1 ; and gapw=32. A Bestfit comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

Uses for the Liver Cancer Markers as Diagnostics As described herein, the genes and gene expression information provided in Tables 3-9 may be used as diagnostic markers for the prediction or identification of the malignant state of the liver tissue. For instance, a liver tissue sample or other sample from a patient may be assayed by any of the methods described herein or by any other method known to those skilled in the art, and the expression levels from a gene or genes from the Tables, in particular the genes in Tables 3-5, may be compared to the expression levels found in normal liver tissue, tissue from metastatic liver cancer or hepatocellular carcinoma tissue.

Expression profiles generated from the tissue or other sample that substantially resemble an expression profile from normal or diseased liver tissue may be used, for instance, to aid in disease diagnosis. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the Liver Cancer Markers for Monitoring Disease Progression As described above, the genes and gene expression information provided in Tables 3-9 may also be used as markers for the monitoring of disease progression, for instance, the development of liver cancer. For instance, a liver tissue sample or other sample from a patient may be assayed by any of the methods described above, and the expression levels in the sample from a gene or genes from or 3-9 may be compared to the expression levels found in normal liver tissue, tissue from metastatic liver cancer or hepatocellular carcinoma tissue. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the Liver Cancer Markers for Drug Screening According to the present invention, the genes identified in Tables 3-9 may be used as markers to evaluate the effects of a candidate drug or agent on a cell, particularly a cell undergoing malignant transformation, for instance, a liver cancer cell or tissue sample. A candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers (drug targets) or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of drugs' effects by looking at the number of markers affected by different drugs and comparing them. More specific drugs will affect fewer transcriptional targets. Similar sets of markers identified for two drugs indicates a similarity of effects.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agents action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites.

For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNA encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see Grant, (1995) in Molecular Biology and Biotechnology Meyers (editor) VCH Publishers). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Assay Formats The genes identified as being differentially expressed in liver cancer may be used in a variety of nucleic acid detection assays to detect or quantitate the expression level of a gene or multiple genes in a given sample. Any hybridization assay format may be used, including solution-based and solid support-based assay formats, for example, traditional Northern blotting. Other suitable assay formats that may be used for detecting gene expression levels include, but are not limited to, nuclease protection, RT-PCR and differential display methods. These methods are useful for some embodiments of the invention; however, methods and assays of the invention are most efficiently designed with array or chip hybridization-based methods for detecting the expression of a large number of genes. Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100,

preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 or more different nucleic acid hybridizations.

Assays to monitor the expression of a marker or markers as defined in Tables 3-9 may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up-or down-regulating expression of the nucleic acid in a cell.

In one assay format, gene chips containing probes to at least two genes from Tables 3-9 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell as described in more detail above. In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the 3' or 5' regulatory regions of a gene in Tables 3-9 and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam et al., (1990) Anal.

Biochem. 188, 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of one or more genes identified in Tables 3-9. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook et al., (1989) Molecular Cloning-A Laboratory Manual, Cold Spring Harbor Laboratory Press).

In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cell and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Such cell lines may be, but are not required to be, derived from liver tissue. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (e. g., a plasmid or viral vector) construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the instant gene products fused to one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct tag. Such a process is well known in the art (see Sambrook et al., (1989) Molecular Cloning-A Laboratory Manual, Cold Spring Harbor Laboratory Press).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (e. g., ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample will be compared with a control sample where only the

excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control will be used to distinguish the effectiveness of the agent.

Another embodiment of the present invention provides methods for identifying agents that modulate the levels, concentration or at least one activity of a protein (s) encoded by the genes in Tables 3-9. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein of the invention between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not and the genes may be amplified or not. The cloning itself does not appear to bias the representation of genes within a population. However, it may be preferable to use polyA<sup>+</sup> RNA as a source, as it can be used with less processing steps.

The sequences of the expression marker genes are in the public databases. Tables 3- 9 provide the Affymetrix gene ID and GenBank accession number for each marker identified. The nucleotide sequence for each marker has been provided in electronic format with this application and these sequences are incorporated herein by reference as are equivalent and related sequences present in the public databases.

Probes based on the sequences of the genes described herein may be prepared by any commonly available method. Oligonucleotide probes for assaying the tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases longer probes of at least 30, 40, or 50 nucleotides will be desirable.

**Probe design** One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of probes that specifically hybridize to the sequences of interest. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, in a preferred embodiment, the array will include one or more control probes.

High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 500 or about 5 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments the probes are about 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using natural nucleic acid as templates.

These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.



In addition to test probes that bind the target nucleic acid (s) of interest, the high density array can contain a number of control probes. The control probes fall into three categories referred to herein as (1) normalization controls; (2) expression level controls; and (3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (e. g., fluorescence intensity) read from all other probes in the array are divided by the signal (e. g., fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control (s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (i. e., no secondary structure) and do not match any target-specific probes.

Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typical expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the P-actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (e. g., stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a twenty-mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (e. g., substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes also indicate whether a hybridization is specific or not. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation. The difference in intensity between the perfect match and the mismatch probe (I (PM)-I (MM)) provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process.

Methods of isolating total mRNA are also well known to those of skill in the art. For example, methods

of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I Theory and Nucleic Acid Preparation, Tijssen, (1993) (editor) Elsevier Press. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and an RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates can be used.

Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised in vitro, such as cell lines and tissue culture cells.

Frequently the sample will be a "clinical sample" which is a sample derived from a patient.

Typical clinical samples include, but are not limited to, sputum, blood, blood-cells (e. g., white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom.

Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

**Solid Supports** Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, silicon or glass based chips, etc.

Such wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755). Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, about 2,10,100,1000 to 10,000; 100,000 or 400,000 of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of a square centimeter.

Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart et al., (1996) Nat.

Biotechnol. 14,1675-1680; McGall et al., (1996) Proc. Nat. Acad. Sci. USA 93,13555- 13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described herein. Such arrays may also contain oligonucleotides that are complementary or hybridize to at least about 2,3, 4,5,6,7,8,9,10,20,30,50,70,100 or or more the genes described herein.

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a solid substrate by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung et al., (1992) U. S. Patent No.

5,143,854; Fodor et al., (1998) U. S. Patent No. 5,800,992; Chee et al., (1998) 5,837,832.

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific

implementation, a glass surface is derivatized with a silane reagent containing a functional group, e. g., a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in Fodor et al., (1993). WO 93/09668. High density nucleic acid arrays can also be fabricated by depositing premade or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

**Hybridization** Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing (see Lockhart et al., (1999) WO 99/32660).

The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids.

Under low stringency conditions (e. g., low temperature and/or high salt) hybrid duplexes (e. g., DNA-DNA, RNA-RNA or RNA-DNA) will form even where the annealed sequences are not perfectly complementary.

Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e. g., higher temperature or lower salt) successful hybridization requires fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. In a preferred embodiment, hybridization is performed at low stringency, in this case in 6x SSPE-T at 37°C (0.005% Triton x-100) to ensure hybridization and then subsequent washes are performed at higher stringency (e. g., 1 x SSPE-T at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (e. g., down to as low as 0.25x SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (e. g., expression level control, normalization control, mismatch controls, etc.).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

**Signal Detection** The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art (see Lockhart et al., (1999) WO 99/32660).

**Databases** The present invention includes relational databases containing sequence information, for instance for the genes of Tables 3-9, as well as gene expression information in various liver tissue samples. Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information, or descriptive information concerning the clinical status of the tissue sample, or the patient from which the sample was derived. The database may be designed to include different parts, for instance a sequences database and a gene expression database.

Methods for the configuration and construction of such databases are widely available, for instance, see Akerblom et al., (1999) U. S. Patent 5,953,727, which is herein incorporated by reference in its entirety.

The databases of the invention may be linked to an outside or external database. In a preferred embodiment, as described in Tables 3-9, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI).

Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such as those available from Silicon Graphics. Client-server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northern blots to allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising at least one gene in Tables 3-9 comprising the step of comparing the expression level of at least one gene in Tables 3-9 in the tissue to the level of expression of the gene in the database. Such methods may be used to predict the physiological state of a given tissue by comparing the level of expression of a gene or genes in Tables 3-9 from a sample to the expression levels found in tissue from normal liver, malignant liver or hepatocellular carcinoma. Such methods may also be used in the drug or agent screening assays as described below.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

**EXAMPLES** Example 1: Tissue Sample Acquisition and Preparation Figure 1 outlines the experimental protocol used. Liver tissue samples were excised and snap frozen in liquid nitrogen. The clinical data for each of the samples included in this study are outlined in Table 1. The sample set was composed of eight samples of normal liver tissue (N1-N8), five samples of metastatic adenocarcinoma arising from rectum (designated M1 and M3) and colon (M2, M4 and M5) tissues and six samples of primary hepatocellular carcinomas. Samples were named according to type of tissue: HCC=hepatocellular carcinoma,

M=metastatic, N=normal. Table 1 includes the TNM classification (the American Joint Committee on Cancer's system of classifying cancers) of the tissues used as samples where T refers to the extent of the primary tumor, N refers to the absence or presence and extent of regional lymph node metastasis, and M refers to the absence or presence of distant metastasis. Numbers following T, N, and M refer to the size of the primary tumor and the amount of vascular invasion, where 0=no evidence of tumor, lymph node involvement or metastasis, 4=multiple tumors involved, and x=cannot be assessed. Histopathologic grade (Table 1) is a qualitative assessment of differentiation of a tumor, where G1=most differentiated and G4=undifferentiated. Clinical stage (Table 1) characterizes the anatomic extent of disease in the patient from whom the sample was taken, where I and II are early stages, III and IV are late stages.

With minor modifications, the sample preparation protocol followed the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was first ground to powder using the Spex Certiprep 6800 Freezer Mill. Total RNA was then extracted using Trizol (Life Technologies). The total RNA yield for each sample (average tissue weight of 300 mg) was 200-500  $\mu$ g. Next, mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen). Since the mRNA was eluted in a final volume of 400  $\mu$ l, an ethanol precipitation step was required to bring the concentration to 1  $\mu$ g/ $\mu$ l. Using 1-5  $\mu$ g of mRNA, double stranded cDNA was created using the SuperScript Choice system (Gibco-BRL). First strand cDNA synthesis was primed with a T7- (dT24) oligonucleotide. The cDNA was then phenol-chloroform extracted and ethanol precipitated to a final concentration of 1  $\mu$ g/ $\mu$ l. From 2  $\mu$ g of cDNA, cRNA was synthesized according to standard procedures. To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. After a 37°C incubation for six hours, the labeled cRNA was cleaned up according to the Rneasy Mini kit protocol (Qiagen). The cRNA was then fragmented (5x fragmentation buffer: 200 mM Tris-Acetate (pH 8.1), 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C.

55  $\mu$ g of fragmented cRNA was hybridized on the human Hu35k set and the HuGeneFL array for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between.

Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Following hybridization and scanning, the microarray images were analyzed for quality control, looking for major chip defects or abnormalities in hybridization signal. After all chips passed QC, the data was analyzed using Affymetrix GeneChip software (v3.0), and Experimental Data Mining Tool (EDMT) software (v1. 0).

**Example 2: Gene Expression Analysis** All samples were prepared as described and hybridized onto the Affymetrix HuGeneFL array and the Human Hu35k set of arrays. Each chip contains 16-20 oligonucleotide probe pairs per gene or cDNA clone. These probe pairs include perfectly matched sets and mismatched sets, both of which are necessary for the calculation of the average difference. The average difference is a measure of the intensity difference for each probe pair, calculated by subtracting the intensity of the mismatch from the intensity of the perfect match. This takes into consideration variability in hybridization among probe pairs and other hybridization artifacts that could affect the fluorescence intensities. Using the average difference value that has been calculated, the GeneChip software then makes an absolute call for each gene or EST.

The absolute call of present, absent or marginal is used to generate a Gene Signature, a tool used to identify those genes that are commonly present or commonly absent in a given sample set, according to the absolute call. For each set of samples, a median average difference was figured using the average differences of each individual sample within the set. The median average difference must be greater than

150 to assure that the expression level is well above the background noise of the hybridization. For the purposes of this study, only the genes and ESTs with a median average difference greater than 150 have been further studied in detail.

The Gene Signature for one set of samples is compared to the Gene Signature of another set of samples to determine the Gene Signature Differential. This comparison identifies the genes that are consistently present in one set of samples and consistently absent in the second set of samples.

The Gene Signature Curve is a graphic view of the number of genes consistently present in a given set of samples as the sample size increases, taking into account the genes commonly expressed among a particular set of samples, and discounting those genes whose expression is variable among those samples. The curve is also indicative of the number of samples necessary to generate an accurate Gene Signature. As the sample number increases, the number of genes common to the sample set decreases. The curve is generated using the positive Gene Signatures of the samples in question, determined by adding one sample at a time to the Gene Signature, beginning with the sample with the smallest number of present genes and adding samples in ascending order. The curve displays the sample size required for the most consistency and the least amount of expression variability from sample to sample. The point where this curve begins to level off represents the minimum number of samples required for the Gene Signature. Graphed on the x-axis is the number of samples in the set, and on the y-axis is the number of genes in the positive Gene Signature.

**Example 3: Gene Expression Analysis of Normal Liver Tissue** The gene expression patterns and Gene Signature were individually determined for each sample set: eight samples with normal liver pathology, six samples whose pathology indicated the primary malignancy to be hepatocellular carcinoma, and five samples whose primary colorectal adenocarcinoma had metastasized to the liver. The Gene Signatures obtained for the normal sample set is shown in Figure 2A, the metastatic liver cancer set in Figure 2B and the hepatocellular carcinoma set in Figure 2C.

The Gene Signature considers the present and absent genes alone, and does not take into consideration those that have been called marginal. Table 2 shows the numbers of present genes, called the positive Gene Signature, and the number of absent genes, called the negative Gene Signature, for each of the three sets of samples.

The Gene Signature is the set of genes that are commonly present or commonly absent in N-1 samples of a given sample set. The positive Gene Signature for the normal liver tissues contains 6,213 genes and ESTs. This same set of normal samples did not show any detectable level of expression of 24,900 genes. Many of the genes and ESTs in this positive Gene Signature are housekeeping genes or structural genes that are not only expressed in the liver, but are ubiquitously expressed in tissues throughout the body. Within this positive Gene Signature are also those genes whose expression is specifically restricted to normal liver tissue and those genes required for the liver to function at its normal capacities. It is the group of genes unique to the liver whose expression levels are most likely to change during tumorigenesis. Whether up-regulated or down-regulated or turned completely on or turned completely off, the changes in expression of these vital genes very likely contributes to the drastic changes in liver function caused by the transformation of normal liver cells into cancerous cells.

**Example 4: Gene Expression Analysis of Malignant Liver Tissue** There are 8,479 genes and ESTs in the positive Gene Signature for the HCC tumors, and a total of 23,233 genes and ESTs are included in the negative Gene Signature of the HCC samples. This negative Gene Signature includes all the genes that have been completely turned off during tumorigenesis, as well as those genes that are not usually expressed in liver tissue. These results include a number of genes and ESTs that are not regularly expressed in liver tissues, but through the process of tumor production, their expression patterns have

been dramatically altered from no detectable level of expression to some significant level of expression in comparison with the normal liver.

The colorectal metastases in the liver commonly express 5,102 genes and ESTs, and do not show expression of 30,455 additional genes and ESTs. As with the negative Gene Signature for the HCC sample set, the genes included in this data set are generally not expressed in liver tissue, whether tumor or normal tissue. The 5,102 in the sample set of metastatic tumors also identify those genes with expression levels that have been changed from off to on as a result of tumor formation.

**Example 5: Analysis of Gene Expression Profiles** A differential comparison of the genes and ESTs expressed in the normals and the two different types of liver tumors identifies a subset of the genes included in the positive Gene Signatures that are uniquely expressed in each sample set. This Gene Signature Differential highlights genes whose expression profiles have most dramatically changed in the transformation from normal to diseased liver cells. The parameters for these analyses were set to accommodate variation in expression of one of eight normal samples and one of the six HCC samples or one of the 5 metastatic tumor samples, such that the genes categorized as unique to normal were called present by the software in seven of eight (87%) normal liver samples and were also called absent in five of six HCC (83%) or four of five (80%) metastatic liver tumor. Conversely, the genes categorized as unique to each set of tumors as compared to the normal livers were called present in five of six HCC (83%) or four of five (80%) metastatic tumor samples and absent in seven of eight normal livers (87%).

The Gene Signature Differential comparing the normal livers to those with metastatic tumors identified a total of 903 sequences expressed only in normal liver tissue.

The number of genes or ESTs that meet the median average difference minimum of 150 is 449, of which 289 are genes and the number of ESTs is 160. The remaining ESTs and genes may be indistinguishable from the background noise of the hybridization. The same comparison of normals versus metastatic tumors demonstrates that in the metastatic tumor samples there are 296 uniquely expressed sequences. Those that meet the median average difference minimum requirement are 83 genes and 72 ESTs. Those genes and ESTs expressed in metastatic and not in normal liver tissue are shown in Table 9A and those present in normal liver tissue and not metastatic tissue Table 9B. Numerous genes with differing expression levels in metastatic liver tumor tissue compared to normal tissue were identified. The fifteen genes whose expression level was most different in metastatic as compared to normal tissue are shown in Table 4. Those with the most increased expression are in Table 4A and those with the most decreased expression are in Table 4B. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. Fold change was calculated as a ratio with a p value given as a measure of statistical significance. Fold change is considered significant for a given gene or EST when it is greater than 3.0 with a p value <0.05. Only the characterized genes have been listed; the ESTs with similar fold changes are not presented here. Asterisk (\*) in Table 4 denotes those genes that were also identified in the Gene Signature differential between metastatic liver carcinoma and normal liver tissue. A complete listing of all the genes and ESTs with at least a three-fold change in expression is shown in Table 6. Table 6A contains those genes and ESTs whose expression level increased in metastatic tissue relative to normal tissue and Table 6B contains those genes and ESTs whose expression level decreased.

The Gene Signature Differential between the normal liver samples and the HCC samples identifies a total of 47 unique expressers in the normals, 23 with an median average difference of 150,13 of which are named gene and 10 of which are ESTs. When comparing the expression of the HCC samples with the normal livers, there are 243 genes and ESTs only expressed in the HCC samples.

Those genes and ESTs expressed in HCC and not in normal liver tissue are shown in Table 8A and those



present in normal liver tissue and not HCC tissue in Table 8B.

Numerous genes with differing expression levels in HCC compared to normal tissue were identified. The fifteen genes whose expression level was most different in HCC as compared to normal tissue are shown in Table 3. Those with the most increased expression are in Table 3A and those with the most decreased expression are in Table 3B. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. Fold change was calculated as a ratio with a p value given as a measure of statistical significance. Fold change is considered significant for a given gene or EST when it is greater than 3.0 with a p value  $<0.05$ . Only the characterized genes have been listed; the ESTs with similar fold changes are not presented here. Asterisk (\*) denotes those genes that were also identified in the Gene Signature differential between hepatocellular carcinoma and normal liver tissue. A complete listing of all the genes and ESTs with at least a three-fold change in expression is shown in Table 7. Table 7A contains those genes and ESTs whose expression level increased in hepatocellular carcinoma tissue relative to normal tissue and Table 7B contains those genes and ESTs whose expression level decreased.

Analysis of sample set identified 24 ESTs and 42 genes that are expressed in both metastatic liver tumors and hepatocellular carcinomas, but not in normal liver tissues. The fifteen genes with the most increase in expression level in both types of cancer are shown in Table 5. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. The mean expression value for HCC and metastatic carcinomas was greater than 250, and included only those genes that showed a fold change greater than 3 with significant p values for both sets of tumors. No detectable level of expression was found in the normal liver tissues for these genes. Only the characterized genes have been listed; the ESTs with similar fold changes that are unique to the tumors are not presented here.

Differential gene expression patterns between normal liver samples and hepatocellular carcinomas and between normal livers and metastatic liver tumors were examined. Genes uniquely expressed by each of the groups individually were identified, as well as those genes that are commonly expressed among liver tumors, whether primary hepatocellular carcinomas or metastatic liver tumors.

**Example 6: Association of Liver Cancer with Specific Gene Expression** The present inventors have closely examined a number of the tumor-expressing genes to determine if their expression patterns correlate with previous reports published in the literature, and to define a logical relationship between the gene and hepatocarcinogenesis. A number of genes that have previously been associated with either liver cancer or other types of cancers were identified, as well as numerous genes that have not been linked to cancers in any previous studies.

842 genes and ESTs that are up-regulated in hepatocellular carcinomas were identified when compared with normal liver tissue. One such gene is PTTG1, pituitary tumor-transforming gene 1, or securin, an oncogene that inhibits sister chromatid separation during anaphase. Normal tissues show little or no PTTG1 expression, but high levels of expression have been associated with various tumors, including liver tumors, and carcinoma cell lines. Overexpression in NIH3T3 cells resulted in transformation, and these cells caused the formation of tumors when injected into mice. The mechanism by which this tumorigenic activity takes place is postulated to be through the missegregation of sister chromatids, resulting in aneuploidy and, therefore, genetic instability. Our data further support this overexpression of PTTG1 in hepatocellular carcinoma, with a fold change of 10.7 ( $P=0.00052$ ), and no detectable level of expression in normal tissues, as identified by the differential comparison of the consensus patterns of gene expression of these two sample sets.

Galectin 3, LGALS3, one of a family of beta-galactoside-binding animal lectins, is significantly

overexpressed both in primary hepatocellular carcinoma and metastatic liver carcinomas with fold changes of 6.8 ( $P=0.00103$ ) and 27.1 ( $P=0.00001$ ), respectively.

Expression of LGALS3 has been associated with tumor growth, progression, and metastasis, as well as cell-cell and cell-matrix interactions and inflammatory processes. Although expression studies by Hsu et al. revealed no detectable level of galectin-3 in normal liver cells, samples from patients with hepatocellular carcinoma revealed considerable levels of LGALS3 expression. The abnormal expression of this lectin may be an early event in the process of transformation of normal cells to tumor cells, or it may impart an increased capacity for these tumor cells to survive and proliferate. Consistent with the reports by Iurisci et al and Nakamura et al, an increased expression level was found in both types of tumor, but higher concentrations of galectin-3 were observed in liver metastases from colorectal tumors than in the primary HCC tumors.

Another gene that is overexpressed in both hepatocellular carcinoma and metastatic colorectal adenocarcinomas with fold changes of 12.2 ( $P=0.00169$ ) and 58.0 ( $P=0.00063$ ), respectively, is solute carrier family 2, member 3, or glucose transporter 3 (GLUT3). It is one of a family of transmembrane proteins that function as facilitative glucose transporters, which has a unique specificity for brain and neuronal tissues. Glucose uptake and metabolism are known to be increased in carcinoma cells compared to normal cells.

Glucose transporter expression may be elevated in response to the increase in glucose utilization seen in actively proliferating cells, like those of tumors. Conversely, the high levels of glucose transporter expression may be responsible for the enhanced influx of glucose into the tumor cells. Various reports have indicated increased expression of one or more of the family of glucose transporters in malignancies, including those of the brain, esophagus, colon, pancreas, liver, breast, lung, bladder, ovary, testis, skin, head and neck, kidney, and gastric tumors. Kurata et al. (Jpn-J Cancer Res 1999 Nov; 90 (11) : 1238-43) specifically report that metastatic liver carcinomas have even higher levels of GLUT3 expression than primary tumors. Consistent with previous studies, the current data confirm the significant overexpression of GLUT3 both in primary liver cancer, hepatocellular carcinoma, and in tumors that have metastasized from the colon and rectum.

One of the significantly underexpressed genes identified by comparing the expression profiles of hepatocellular carcinomas and metastatic liver tumors with that of normal liver tissue is metallothionein 1L. The expression level in HCC is 26.9 fold lower than that of normal ( $P=0.00999$ ), and in metastatic colorectal adenocarcinomas it is down-regulated 66.5 fold ( $P=0.00415$ ). Metallothioneins are heavy metal binding proteins that are involved in detoxification of metals, zinc and copper metabolism cellular adaptation mechanisms, and may be involved in regulating apoptosis. Colorectal adenocarcinoma that has metastasized to the liver has been specifically reported to express less metallothionein than normal liver tissue. Comparison of the consensus patterns of gene expression between metastatic liver samples and normal liver samples show no significant level of MT1L expression in the tumors. Furthermore, additional work has determined that human hepatocellular carcinomas contain much lower levels of metallothioneins than normal liver tissue, and that this decrease correlates with the degree of differentiation and concentrations of copper and zinc in the cells. By comparing the expression profiles of hepatocellular carcinoma and normal liver tissue, this significant reduction in MT1L expression in HCC was confirmed.

A number of enzymes belonging to the family of cytochrome P450s are drastically underexpressed in the two sets of liver tumors in comparison with the normal liver tissue.

For example, expression of CYP2A6 is decreased in HCC with a fold change of 14.2 ( $P=0.0307$ ), and in metastatic tumors with a fold change of 69.9 ( $P=0$ ). CYP8B1 is down-regulated 19.3 fold ( $P=0.00807$ )

in HCC and 65.1 fold ( $P=0.0039$ ) in liver metastases. In addition to these commonly down-regulated cytochrome P450s, in HCC samples CYP2B is underexpressed 17.9 fold ( $P=0.01469$ ), and in the metastatic liver tumors CYP2C9 and CYP2A7 are underexpressed 84.7 fold ( $P=0.00327$ ) and 72.0 fold ( $P=0$ ), respectively.

Several of these genes are also identified by the differential comparison between expression profiles of tumor and normal, confirming the significant decrease in expression in tumor tissues. Many of these P450 enzymes are critical players in the metabolism of carcinogens, drugs, and other chemical compounds, that are expressed in normal liver.

In addition to genes that are underexpressed in metastatic adenocarcinomas in the liver, more than 1000 genes and ESTs that are overexpressed specifically in these tumors were identified. Two of the most highly up-regulated are claudin 4, also known as clostridium perfringens enterotoxin receptor 1 (fold change 84.4,  $P=0$ ) and occludin (fold change 43.1,  $P=0$ ). Both of these genes are tight junction proteins, responsible for the formation and maintenance of continuous seals around epithelial cells to form a physical barrier that blocks the free passage of water and solutes through the paracellular space.

More specifically, claudin-4 is one member of a family of transmembrane proteins that comprise tight junction strands, and occludin is a cell adhesion molecule (Morita et al., (1999) Proc. Natl. Acad. Sci. U. S. A. 96: 511-516). Claudins likely function as paracellular channels, regulating the flow of ions and solutes into and out of the paracellular space (Simon et al., (1999) Science 285: 103-106; Wong & Goodenough (1999) Science 285: 62; Anderson & Van Itallie (1999) Curr. Biol. 9: R922-924). Tight junction proteins also contribute to the regulation of the cellular processes of cell growth and differentiation (Matter & Balda (1999) Int. Rev. Cytol. 186: 117-146). Permeability of tight junctions has been associated with tumor formation, where a breakdown in the barrier function of tight junctions allows an increase in the cellular permeability. This breakdown then opens the tight junction barrier, permitting invasion by tumor cells (Zak et al., (2000) Pflugers Arch.

440: 179-183; Mullin (1997) J. Exp. Zool. 279: 484-489). It has been reported that tight junctions of colon tumors leak more than do the tight junctions of normal colon (Soler et al., (1999) Carcinogenesis 20: 1425-1431). A complete loss of tight junction function and a loss of cell-cell contact growth control was seen in cells that had been transfected with oncogenic Raf-1, and expression levels of occludin and another claudin are lower in these cells (Li & Morsny (2000) J. Cell Biol. 148: 791-800). Occludin expression has been up-regulated in vitro by the addition of various fatty acids that have anti-cancer effects, decreasing the paracellular permeability (Jiang et al., (1998) Biochem. Biophys. Res.

Commun. 244: 414-420). The extreme down-regulation of occludin and claudin-4 in metastatic liver tumors is strongly supported by the reports of tight junction breakdown in tumor tissues.

The present study identified 93 significantly up-regulated genes in both primary HCC and metastatic liver tumors that were not found to have any detectable level of expression in the normal samples. Serine protease inhibitor, Kazal type I (SPINK1), also called pancreatic secretory trypsin inhibitor (PSTI) or tumor-associated trypsin inhibitor (TATI), is one such gene. It is highly expressed in the cells of normal pancreas and in the mucosa of the gastrointestinal tract where it offers protection from proteolytic breakdown.

A marked increase in expression is seen in various pancreatic diseases and in tumors of different tissues, including gastric carcinomas, colorectal cancers, and other neoplastic tissues. This increase is presumably due to the elevated expression of trypsin in the tumors, and not related to amplification or rearrangements within the gene. SPINK1 is also considered a valuable marker for a number of solid

tumors. A drastic elevation of SPEK1 in the blood of patients with hepatocellular carcinoma has been seen (see Ohmachi et al.).

Furthermore, it has been suggested that the level of expression correlates with the extent of tumor, such that this heightened expression level could be indicative of HCC under certain conditions. In keeping with this report of overexpression in these tumors, the present expression data show the levels of expression of this gene in HCC samples to be 28.9 times higher than normal ( $P=0.00003$ ), and in metastatic liver tumors the expression level is 9.8 times higher than normal ( $P=0.03697$ ).

Midkine is one of a family of heparin-binding growth factors, inducible by retinoic acid, and is actively involved in cell-cell interactions and angiogenesis. The expression pattern of midkine is highly restricted in normal adult tissues, and no expression has been reported in normal adult liver, although its expression is required during embryogenesis for normal development. However, it is expressed in moderate to high levels in many tumors, including Wilm's tumors of the kidney, stomach, colon, pancreas, lung, esophagus, breast, and liver tumors. The present data confirm these reports, showing a significant overexpression of midkine in hepatocellular carcinoma samples (fold change 9.9,  $P=0.02104$ ) and in liver metastases (fold change 10.4,  $P=0.01818$ ), but no noticeable expression in normal liver.

Stathmin, leukemia-associated phosphoprotein 18, is a phosphoprotein whose expression pattern and phosphorylation status are controlled by extracellular signals responsible for the regulation of the processes of cell proliferation and differentiation. It is also involved in the regulation of cell division via the destabilization of microtubules.

When comparing expression levels between non-malignant tissues and malignant tissues, the tumors generally show a significant up-regulation of this phosphoprotein, specifically lymphomas, leukemias, breast and prostate tumors. One reason proposed for this elevated expression in cancer cells is the dissimilarity in the rates of cell proliferation and states of differentiation between normal and tumor cells. In both HCC samples and metastatic adenocarcinomas, significant up-regulation of stathmin, 9.4 fold in HCC ( $P=0.00015$ ) and 4.8 fold in metastatic tumors ( $P=0.00514$ ) was seen.

Both the genes and ESTs described here will provide valuable information for the identification of new drug targets against liver carcinomas, and that information may be extended for use in the study of carcinogenesis in other tissues.

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, applications and publications referred to in this application are herein incorporated by reference in their entirety.

Table 1. Clinical Information for Hepatocellular Carcinoma, Metastatic Liver Tumor, and Normal Liver Samples Included in this Study

Sample	Pathology	Primary Tumor	Age	Gender	Race	TNM
H1	Hepatocellular Carcinoma	Liver	64	Male	Caucasian	T3, Nx, Mx G2 stage III
H2	Hepatocellular Carcinoma	Liver	27	Female	Caucasian	T3, No, Mx G1 stage III
H3	Hepatocellular Carcinoma	Liver	78	Female	Caucasian	T4, Nx, Mx G2 stage III
H4	Hepatocellular Carcinoma	Liver	43	Male	Asioan	T4, N1, Mx G2 stage IV
H5	Hepatocellular Carcinoma	Liver	51	Male	Caucasian	T4, No, Mx G2 stage IV
H6	Hepatocellular Carcinoma	Liver	57	Male	Caucasian	unavailable G2 stage III
M1	Metastatic Adenocarcinoma	Rectum	61	Female	Caucasian	Tx, Nx, M1 G3 stage IV; Duke D
M2	Metastatic Adenocarcinoma	Colon	54	Male	Caucasian	unavailable G2 stage IV; Duke D
M3	Metastatic Adenocarcinoma	Rectum	50	Female		

Caucasian Tx,Nx,M1 G2 stage IV; Duke D M4 Metastatic Adenocarcinoma Colon 60 Male Caucasian Tx,Nx,M1 G2 stage IV; Duke D M5 Metastatic Adenocarcinoma Colon 57 Male Caucasian Tx,Nx,M1 G2 stage IV; Duke D N1 Normal liver 54 Female Caucasian N2 Normal liver 55 Female Caucasian N3 Normal liver 58 Male Caucasian N4 Normal liver 44 Female Caucasian N5 Normal liver 40 Female Caucasian N6 Normal liver 72 Female Caucasian N7 Normal liver 48 Female Unknown N8 Normal liver 55 Female Caucasian Table 2. Summary of genes and ESTs Expressed in HCC, Metastatic Liver Tumors, and Normal Livers Hepatocellular Colorectal Normal Livers Carcinoma Metastases I. Fingerprint of Gene Expression Genes and ESTs commonly expressed in sample set 8479 5102 6213 Genes and ESTs commonly unexpressed in sample set 23233 30455 24900 II. Fold Change Genes and ESTs overexpressed in tumors (fold change >3 and  $p < 0.05$ ) 842 1044 Number of Genes 430 603 Number of ESTs 412 441 Genes and ESTs underexpressed in tumors (fold change >3 and  $p < 0.05$ ) 393 1867 Number of Genes 235 1016 Number of ESTs 158 851 III. Differential Comparison between Normal and Tumor Expression Genes and ESTs turned ON in tumors 243 296 Genes and ESTs with expression level above threshold in tumor 77 155 Number of Genes 38 83 Number of ESTs 39 72 Genes and ESTs turned OFF in tumors 47 903 Genes and ESTs with expression level above threshold in normal 23 449 Number of Genes 13 289 Number of ESTs 10 160 Table 3A. Top fifteen genes overexpressed in hepatocellular carcinoma.<BR> <P>Genbank Seq ID Unigene Cluster Gene Name Fold Change Pvalue<BR> AA055896 135 Hs.146428 collagen, type V, alpha 1 10.9\* 0.000907<BR> AA156187 339 Hs.81634 ATP synthase, H<sup>+</sup> transporting, mitochondrial F0 complex, subunit b, isoform 1 9.4 0.02007<BR> AA428172 986 Hs.8546 Notch (Drosophila) homolog 3 9.6\* 0.00195<BR> AA430032 1009 Hs.252587 pituitary tumor-transforming 1 10.7\* 0.00052<BR> AA505133 1417 Hs.279905 solute carrier family 2 (facilitated glucose transporter), member 3 12.2 0.00169<BR> AA610116 1499 Hs.102737 tetraspan NET-6 protein 16.4 0.00249<BR> AA620881 1510 Hs.21858 trinucleotide repeat containing 3 9.5 0.00062<BR> D31094 1639 Hs.109798 G8 protein 9.4 0.0048<BR> D51276 1678 Hs.81915 leukemia-associated phosphoprotein p18 (stathmin) 9.4 0.00015<BR> J03464 2094 Hs.179573 collagen, type I, alpha 2 10.4 0.00979<BR> M94250 2426 Hs.82045 midkine (neurite growth-promoting factor 2) 9.9\* 0.02104<BR> N33920 2493 Hs.44532 diubiquitin 50.3 0<BR> W45320 3523 Hs.228059 KRAB-associated protein 1 10.1\* 0.00002<BR> Y00705 3850 Hs.181286 serine protease inhibitor, Kazal type 1 28.9 0.00003<BR> Z37987 3882 Hs.119651 glypican 3 10.7 0.02304 Table 3B. Top fifteen genes underexpressed in hepatocellular carcinoma.<BR> <P>Genbank Seq ID Unigene Cluster Gene Name Fold Change Pvalue<BR> AA007395 17 Hs.1219 alcohol dehydrogenase 4 (class II), pi polypeptide 37.8 0.00939<BR> AA010605 26 Hs.2899 4-hydroxyphenylpyruvate dioxygenase 25.5 0.00855<BR> AA448002 1113 Hs.23759 putative type II membrane protein 14.1\* 0<BR> H58692 1960 Hs.9520 formyltetrahydrofolate dehydrogenase 20.2 0.00485<BR> H80901 2005 Hs.272576 ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen) 18.6 0<BR> H81070 2006 Hs.8765 RNA helicase-related protein 39.6 0.00002<BR> K03192 2127 Hs/183584 cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 14.2 0.0307<BR> M29873 2318 Hs.1360 cytochrome P450, subfamily IIB (phenobarbital-inducible) 17.9 0.01469<BR> N80129 2703 Hs.94360 metallothionein 1L 26.9 0.00999<BR> R97419 3004 Hs.35718 cytochrome P450, subfamily VIIIB (sterol 12-alpha-hydroxylase), polypeptide 1 19.3 0.00807<BR> T48075 3130 Hs.251577 hemoglobin, alpha 1 35.8 0.00471<BR> T67931 3184 Hs.7645 fibrinogen, B beta polypeptide 17.3 0.00128<BR> T95813 3262 Hs.137476 KIAA1051 protein 20.4 0.01361<BR> U56814 3393 Hs.88646 deoxyribonuclease I-like 3 17.7 0.00007<BR> W88946 3639 Hs.18508 putative glycine-N-acyltransferase 25.3 0.00221 Table 4A. Top fifteen genes overexpressed in metastatic carcinomas of the liver.<BR> <P>Genbank Seq ID Unigene Cluster Gene Name Fold Change Pvalue<BR> AA100719 212 Hs.73848 Carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific 50.9\* 0.00081<BR> cross reacting antigen)<BR> AA156243 340 Hs.154737 Serine protease, umbilical endothelium 41.4\* 0.00139<BR> AA335191 741 Hs.173724 Creatine kinase, brain 47.4\* 0.00419<BR> AA421562 934 Hs.91011 Anterior gradient 2 (Xenopus leavis) homolog 56.3\* 0.0041<BR> AA427468 973 Hs.5372 Claudin 4 84.4\* 0<BR> AA429009 994 Hs.233950 Serine protease inhibitor, Kunitz type 1 30.0\* 0.00001<BR> AA610116

1499 Hs.102737 Tetraspan NET-6 protein 33.7 0.00171<BR> H58873 1961 Hs.169902 Solute carrier family 2 (facilitated glucose transporter), member 3 58.0\* 0.00063<BR> H94471 2042 Hs.171952 Occludin 43.1 0<BR> H95233 2048 Hs.31439 Serine protease inhibitor, Kunitz type, 2 47.1 0<BR> HG2788-HT2896 Hs.27258 Calcyclin binding protein 33.2 0<BR> M29540 2317 Hs.220529 Carcinoembryonic antigen-related cell adhesion molecule 5 36.6\* 0.0116<BR> M35252 2343 Hs.84072 Transmembrane 4 superfamily member 3 39.1 0<BR> N92934 2725 Hs.17409 Cysteine-rich protein 1 (intestinal) 35.5 0.002<BR> X93036 3830 Hs.92323 FXYD domain-containing ion transport regulator 3 42.4\* 0.00167 Table 4B. Top fifteen genes underexpressed in metastatic carcinoma of the liver.<BR> <P>Genbank Seq ID Unigene Cluster Gene Name Fold Change Pvalue<BR> AA256367 579 Hs.107966 Paraoxonase 3 70.3 0.00192<BR> H58692 1960 Hs.9520 Formyltetrahydrofolate dehydrogenase 81.4\* 0<BR> K03192 2127 Hs.183584 Cytochrome P450, subfamily IIA(phenobarbital-inducible), polypeptide 6 69.9\* 0<BR> L16883 2166 Hs.167529 Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9 84.7 0.00327<BR> M15656 2268 Hs.234234 Aldolase B, fructose-bisphosphate 96.7\* 0<BR> M16594 2272 Hs.89552 glutathione S-transferase A2 73.2\* 0<BR> M81349 2405 Hs.1955 Serum amyloid A4, constitutive 76.2 0.00015<BR> N53031 2556 Hs.89691 UDP glycosyltransferase 2 family, polypeptide B4 97.6 0.00022<BR> N54417 2567 Hs.90765 Fibrinogen, A alpha polypeptide 99.3 0.00001<BR> R43174 2848 Hs.1898 Paraoxonase 1 74.0\* 0.00038<BR> R49459 2882 Hs.63758 Transferrin receptor 2 85.6 0.00048<BR> T48039 3129 Hs.2351 Protein C (inactivator of coagulation factors Va and VIIIa) 84.4 0.00112<BR> T59148 3158 Hs.50966 Carbamoyl-phosphate synthetase 1, mitochondrial 88.9\* 0<BR> U22029 3327 Hs.250615 Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 72.0\* 0<BR> X55283 3734 Hs.1259 Asialoglycoprotein receptor 2 85 0.00084 Table 5. Top fifteen genes expressed in both hepatocellular carcinomas and metastatic liver tumors ad not in normal livers.<BR> <P>Genbank Seq ID Unigene Cluster Gene Name HCC Fold HCC p Metastatics Metastatic<BR> Change value Fold p value<BR> Change<BR> AA055896 135 Hs.146428 collagen, type V, alpha 1 10.9 0.00907 18.2 0.00146<BR> AA204927 425 Hs.77899 tropomyosin 1 (alpha) 6.1 0.0014 7.1 0.00074<BR> AA335191 741 Hs.173724 creatine kinase, brain 6.5 0.01462 47.4 0.00419<BR> AA429472 997 Hs.236522 DKFZP434P106 protein 8.8 0.00063 8.3 0.00208<BR> AA434418 1036 Hs.72172 KIAA1115 protein 6.8 0.0032 5.1 0.00498<BR> AA452724 1149 Hs.166468 programmed cell death 5 7.7 0.00085 7.2 0.00908<BR> AA610116 1499 Hs.102737 tetraspan NET-6 protein 16.4 0.00249 33.7 0.00171<BR> AA620881 1510 Hs.21858 trinucleotide repeat containing 3 9.5 0.00062 8.7 0.00735<BR> D26129 1635 Hs.78224 ribonuclease, RNase A family, 1 (pancreatic) 6.9 0.00008 5.7 0.03827<BR> D31094 1639 Hs.109798 G8 protein 9.4 0.0048 4.4 0.04845<BR> D51276 1678 Hs.81915 leukemia-associated phosphoprotein p18 (stathmin) 9.4 0.00015 4.8 0.00514<BR> H27188 1908 Hs.9930 collagen-binding protein 2 (collagen 2) 5.8 0.01826 4.2 0.02073<BR> J03464 2094 Hs.179573 collagen, type I, alpha 2 10.4 0.00979 9.8 0.00028<BR> M94250 2426 Hs.82045 midkine (neurite growth-promoting factor 2) 9.9 0.02104 10.4 0.01818<BR> Y00705 3850 Hs.181286 serine protease inhibitor, Kazal type 1 28.9 0.0003 9.8 0.03697 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA001409\_i\_at AA001409 1 EST 3.35 up 0.04092<BR> rc\_AA001504\_f\_at AA001504 2 EST 9.98 up 0.00336<BR> rc\_AA007158\_f\_at AA007158 15 EST 3.05 up 0.01964<BR> rc\_AA007160\_at AA007160 16 EST 6 up 0.01035<BR> rc\_AA010065\_s\_at AA010065 22 CDC28 protein kinase 2 6.25 up 0.02752<BR> rc\_AA011134\_at AA011134 29 EST 28.79 up 0.00602<BR> rc\_AA011383\_at AA011383 31 EST 5.17 up 0.00008<BR> rc\_AA025166\_s\_at AA025166 50 fusion, derived from t (12;16) malignant liposarcoma 3.71 up 0.0052<BR> rc\_AA025277\_at AA025277 51 EST 4.56 up 0.03136<BR> rc\_AA026030\_at AA026030 53 EST 11.01 up 0.01649<BR> rc\_AA026092\_at AA026092 54 EST 3.83 up 0.04596<BR> rc\_AA026150\_at AA026150 55 EST 5.14 up 0.01072<BR> rc\_AA026356\_at AA026356 57 EST 4.1 up 0.00133<BR> rc\_AA027946\_at AA027946 60 EST 3.22 up 0.00098<BR> rc\_AA028103\_at AA028103 61 EST 3.52 up 0.01142<BR> rc\_AA028132\_s\_at AA028132 62 EST 6.25 up 0.00646<BR> rc\_AA029215\_at AA029215 64 adaptor-related protein complex 2, beta 1 subunit 3.65 up 0.00037<BR> rc\_AA029356\_at AA029356 66 EST 3.68 up



0.01545<BR> rc\_AA033790\_f\_at AA033790 74 apolipoprotein D 4.21 up 0.03247<BR>  
 rc\_AA034378\_f\_at AA034378 77 endogenous retroviral protease 4.01 up 0.00974<BR>  
 rc\_AA034499\_s\_at AA034499 78 zinc finger protein 198 3.7 up 0.02143<BR> rc\_AA040465\_at  
 AA040465 95 EST 3.25 up 0.00146<BR> rc\_AA043959\_at AA043959 101 tropomyosin 4 8.54 up  
 0.00222<BR> rc\_AA053007\_f\_at AA053007 123 putative receptor protein 6.76 up 0.00061<BR>  
 rc\_AA053033\_at AA053033 124 EST 7.83 up 0.00379<BR> rc\_AA053102\_s\_at AA053102 125  
 cadherin 17, LI cadherin (liver-intestine) 26.63 up 0.01745<BR> rc\_AA053248\_i\_at AA053248 126  
 EST 7.01 up 0.00003<BR> rc\_AA053248\_f\_at AA053248 126 EST 6.16 up 0.00191<BR>  
 rc\_AA053424\_at AA053424 127 EST 8.76 up 0.01775<BR> rc\_AA053660\_at AA053660 128 EST  
 15.98 up 0.00003<BR> rc\_AA055805\_s\_at AA055805 132 EST 42.83 up 0.00142 Table 6A. Genes up  
 regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known  
 Gene Name Fold Change Direction Pvalue<BR> rc\_AA055811\_s\_at AA055811 133 glycoprotein A33  
 (transmembrane) 6.86 up 0.02152<BR> rc\_AA055896\_at AA055896 135 collagen, type V, alpha 1  
 18.16 up 0.00146<BR> AA056361\_at AA056361 140 integral membrane protein 2C 3.53 up  
 0.02983<BR> rc\_AA062721\_at AA062721 146 nuclear factor (erythroid-derived 2)-like 1 6.2 up  
 0.00024<BR> rc\_AA070206\_at AA070206 155 EST 4.26 up 0.00018<BR> rc\_AA070827\_at  
 AA070827 157 EST 4.41 up 0.01902<BR> rc\_AA074514\_at AA074514 160 EST 7.69 up 0<BR>  
 rc\_AA075299\_at AA075299 164 EST 34.27 up 0.00002<BR> rc\_AA075580\_f\_at AA075580 165 EST  
 4.98 up 0.02083<BR> rc\_AA075722\_at AA075722 166 nuclear transport factor 2 (placental protein 15)  
 4.14 up 0.00374<BR> AA078862\_s\_at AA078862 173 EST 6.52 up 0.00025<BR> rc\_AA084901\_at  
 AA084901 181 ribosomal protein S6 kinase, 70kD, polypeptide 2 9.13 up 0.00003<BR>  
 rc\_AA084921\_f\_at AA084921 182 ribosomal protein S10 3.29 up 0.04872<BR> kangai 1 (suppression  
 of tumorigenicity 6, prostate; CD82<BR> antigen (R2 leukocyte antigen, antigen detected by  
 monoclonal<BR> rc\_AA086232\_f\_at AA086232 186 and antibody 1A4)) 5.14 up 0.01916<BR>  
 AA093497\_s\_at AA093497 199 DEK oncogene (DNA binding) 5.6 up 0.02551<BR> AA094517\_at  
 AA094517 202 EST 3.52 up 0.04805<BR> AA094752\_at AA094752 203 hypothetical 43.2 Kd protein  
 4.47 up 0.00243<BR> rc\_AA099404\_s\_at AA099404 208 EST 29.07 up 0<BR> carcinoembryonic  
 antigen-related cell adhesion molecule 6 (non<BR> rc\_AA100719\_s\_at AA100719 212 specific cross  
 reacting antigen) 50.88 up 0.00081<BR> rc\_AA101551\_at AA101551 216 EST 24.78 up 0<BR>  
 rc\_AA113149\_s\_at AA113149 226 tumor suppressing subtransferable candidate 3 10.58 up  
 0.00543<BR> rc\_AA113303\_at AA113303 227 transmembrane 4 superfamily member (tetraspan NET-  
 7) 3.73 up 0.00084<BR> rc\_AA116036\_at AA116036 233 chromosome 20 open reading frame 1 8.81  
 up 0.00133<BR> rc\_AA121315\_at AA121315 237 KIAA1077 protein 4.86 up 0.02438<BR>  
 rc\_AA122386\_at AA122386 239 collagen, type V, alpha 2 4.28 up 0.005<BR> rc\_AA126044\_at  
 AA126044 245 EST 11.23 up 0.00041<BR> rc\_AA126429\_at AA126429 247 peroxisomal farnesylated  
 protein 3.23 up 0.00478 Table 6A. Genes up regulated in metastatic tissue versus normal sample set  
 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR>  
 rc\_AA126459\_s\_at AA126459 248 DKFZP566B023 protein 3.69 up 0.00352<BR> rc\_AA126719\_at  
 AA126719 250 EST 5.31 up 0.00026<BR> AA127712\_at AA127712 255 EST 6.59 up 0.03706<BR>  
 rc\_AA127851\_at AA127851 257 EST 3.23 up 0.01943<BR> rc\_AA128407\_at AA128407 259 EST  
 3.78 up 0.01081<BR> rc\_AA128561\_at AA128561 261 collagen, type XVII, alpha 1 6.09 up  
 0.0433<BR> rc\_AA131084\_at AA131084 265 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 4.74  
 up 0.00427<BR> rc\_AA131162\_s\_at AA131162 266 EST 4.68 up 0.00042<BR> rc\_AA131584\_at  
 AA131584 268 DKFZP564O0463 protein 6.83 up 0.00025<BR> rc\_AA131894\_at AA131894 269 EST  
 3.76 up 0.00384<BR> rc\_AA131919\_at AA131919 270 putative type II membrane protein 15.36 up  
 0.00027<BR> rc\_AA132032\_s\_at AA132032 271 trinucleotide repeat containing 1 4.19 up  
 0.00295<BR> rc\_AA132554\_at AA132554 273 EST 4.96 up 0.02076<BR> rc\_AA132983\_at  
 AA132983 274 DKFZP586G1517 protein 3.31 up 0.01155<BR> rc\_AA132986\_at AA132986 275 EST  
 9.47 up 0.00552<BR> rc\_AA133590\_at AA133590 282 EST 3.23 up 0.03565<BR> rc\_AA133936\_at  
 AA133936 284 EST 9.19 up 0.00088<BR> rc\_AA134052\_s\_at AA134052 285 Rab  
 geranylgeranyltransferase, alpha subunit 3.54 up 0.03062<BR> rc\_AA134158\_s\_at AA134158 287 EST



3.42 up 0.0277<BR> rc\_AA134968\_at AA134968 289 EST 12.11 up 0.00079<BR> rc\_AA134985\_at AA134985 290 EST 12.11 up 0.00318<BR> rc\_AA135407\_f\_at AA135407 292 endogenous retroviral protease 3.64 up 0.01086<BR> rc\_AA135871\_at AA135871 294 EST 3.39 up 0.01544<BR> rc\_AA135894\_at AA135894 295 retinoic acid induced 3 14.27 up 0.00558<BR> rc\_AA136547\_at AA136547 302 EST 3.51 up 0.00308<BR> rc\_AA143493\_at AA143493 310 pleckstrin 2 (mouse) homolog 4.58 up 0.01037<BR> rc\_AA143763\_at AA143763 311 EST 18.09 up 0.00347<BR> rc\_AA146619\_at AA146619 312 EST 4.87 up 0.00863<BR> rc\_AA147084\_at AA147084 314 proliferation-associated 2G4, 38kD 4.4 up 0.0045<BR> rc\_AA147439\_s\_at AA147439 315 EST 5.01 up 0.00336 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA148885\_at AA148885 320 minichromosome maintenance deficient (S. cerevisiae) 4 6.39 up 0.0125<BR> rc\_AA148977\_at AA148977 322 ESTr 3.64 up 0.02911<BR> rc\_AA149889\_at AA149889 326 neighbor of A-kinase anchoring protein 95 3.34 up 0.02054<BR> rc\_AA150053\_at AA150053 327 EST 3.71 up 0.00102<BR> rc\_AA151182\_at AA151182 332 EST 3.51 up 0.00043<BR> rc\_AA151428\_s\_at AA151428 335 matrix metalloproteinase 23B 7.15 up 0.00056<BR> rc\_AA151778\_at AA151778 338 claudin 7 5.77 up 0.00002<BR> ATP synthase, H<sup>+</sup> transporting, mitochondrial F<sub>0</sub> complex, up<BR> rc\_AA156187\_at AA156187 339 ESTsubunit b, isoform 1 23.24 up 0.00006<BR> rc\_AA156243\_at AA156243 340 serine protease, umbilical endothelium 41.44 up 0.00139<BR> rc\_AA156450\_at AA156450 342 EST 3.33 up 0.00587<BR> rc\_AA157818\_f\_at AA157818 349 endogenous retroviral protease 25.99 up 0.00153<BR> rc\_AA158234\_at AA158234 351 EST 17.04 up 0.00711<BR> rc\_AA158795\_at AA158795 352 EST 3.07 up 0.00057<BR> rc\_AA159525\_at AA159525 354 EST 49.39 up 0.00062<BR> rc\_AA161043\_at AA161043 356 tetraspan 1 18.8 up 0.00015<BR> rc\_AA161292\_s\_at AA161292 357 interferon, alpha-inducible protein 27 13.84 up 0.00004<BR> rc\_AA164252\_f\_at AA164252 358 VGF nerve growth factor inducible 3.41 up 0.00154<BR> NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) up<BR> rc\_AA169837\_at AA169837 364 (NADH-coenzyme Q reductase) 3.17 up 0.03038<BR> rc\_AA171760\_at AA171760 367 EST 17.86 up 0<BR> rc\_AA171939\_at AA171939 368 EST 4.67 up 0.00104<BR> rc\_AA172076\_at AA172076 369 EST 3.06 up 0.00326<BR> rc\_AA173430\_at AA173430 371 EST 4.32 up 0.04362<BR> rc\_AA179298\_at AA179298 378 stomatin-like protein 2 3.72 up 0.00299<BR> rc\_AA179787\_at AA179787 380 polyglutamine binding protein 1 6.44 up 0.00206<BR> rc\_AA179845\_at AA179845 381 EST 5.77 up 0.01414<BR> rc\_AA181600\_at AA181600 384 EST 5.38 up 0.03316<BR> rc\_AA182001\_i\_at AA182001 386 EST 3.56 up 0.00945<BR> rc\_AA187938\_at AA187938 391 EST 3.86 up 0.00512 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq Id known Gene Name Flod Chang Direction Pvalue<BR> rc\_AA18838\_i\_at AA188378 392 EST 9.56 up 0.00271<BR> rc\_AA188378\_f\_at AA188378 392 EST 5.54 up 0.01359<BR> rc\_AA189015\_at AA189015 394 EST 5.27 up 0.00004<BR> rc\_AAS191708\_at AA191708 400 EST 3.87 up 0.01904<BR> rc\_AA192755\_at AA192755 401 EST 3.13 up 0.00442<BR> rc\_AA194237\_at AA194237 408 EST 3.13 up 0.00212<BR> rc\_AA194724\_at AA194724 409 endonuclease G 3.09 up 0.04011<BR> rc\_AA196790\_at AA196790 421 EST 7.64 up 0.00287<BR> rc\_AA204927\_at AA204927 425 tropomyosin 1 (alpha) 7.09 up 0.0074<BR> rc\_AA211483\_at AA211483 435 EST 44.07 up 0.00175<BR> rc\_AA2211851\_f\_at AA2211851 436 EST 3.66 up 0.00789<BR> rc\_AA213696\_at AA213696 437 poly(A)-binding protein, cytoplasmic 1 24.65 up 0.00001<BR> AA215299\_s\_at AA215299 439 U6 snRNA-associated Sm-like protein LSm7 15.84 up 0.00001<BR> rc\_AA215468\_s\_at AA215468 441 ADP-ribosylation factor-related protein 1 3.9 up 0.04549<BR> rc\_AA218663\_at AA218663 444 acid-inducible phosphoprotein 3.26 up 0.0357<BR> AA224502\_at AA224502 451 EST 4.12 up 0.0694<BR> rc\_AA226932\_at AA226932 453 DKFZP564F0923 protein 6.84 up 0.00405<BR> rc\_AA227560\_at AA227560 458 EST 12.81 up 0.01693<BR> rc\_AA227926\_at AA227926 460 EST 6.81 up 0.01701<BR> rc\_AA233886\_s\_at AA233886 475 D site of albumin promoter (albumin D-box) binding protein 3.38 up 0.0218<BR> rc\_AA233959\_i\_at AA233959 477 EST 19.69 up 0.00101<BR> rc\_AA234096\_at AA234096 479 EST 23.72 up 0.00018<BR> rc\_AA23462\_at

AA234362 481 EST 3.89 up 0.03524<BR> rc\_AA235707\_at AA235707 500 ST 9.17 up 0.00005<BR> rc\_AA236037\_at AA236037 506 EST 5.74 up 0.0091<BR> rc\_AA236533\_s\_at AA236533 514 ecotropic viral integration site 1 4.1 up 0.02882<BR> rc\_AA236714\_f\_at AA236714 516 nuclear mitotic apparatus protein 1 4.35 up 0.00083<BR> rc\_AA237017\_at AA237017 521 KIAA 1068 protein 3.52 up 0.00976<BR> rc\_AA243133\_at AA243133 525 serine/threonine kinase 15 7.73 up 0.04328<BR> rc\_AA243173\_at AA243173 526 EST 8.75 up 0.00003 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> AA249819\_s\_at AA249819 535 EST 5.09 up 0.00136<BR> rc\_AA251230\_at AA251230 540 EST 4.75 up 0.00054<BR> rc\_AA251299\_s\_at AA251299 541 KIAA0014 gene product 16.86 up 0.00046<BR> rc\_AA251909\_at AA251909 549 EST 3.35 up 0.03937<BR> rc\_AA252994\_at AA252994 557 apoptosis inhibitor 4 (survivin) 3.55 up 0.00075<BR> rc\_AA253011\_f\_at AA253011 558 KIAA0713 protein 4.73 up 0.01944<BR> AA253330\_s\_at AA253330 562 adaptor-related protein complex 1, gamma 1 subunit 3.87 up 0.00708<BR> rc\_AA253473\_at AA253473 567 EST 15.23 up 0.00171<BR> rc\_AA256273\_at AA256273 577 EST 4.13 up 0.03874<BR> rc\_AA256642\_at AA256642 582 EST 11.17 up 0.00035<BR> rc\_AA258482\_s\_at AA258482 596 zinc finger protein 3.17 up 0.04606<BR> rc\_AA261907\_at AA261907 603 DKFZP566E144 protein 4.54 up 0.02289<BR> rc\_AA262477\_at AA262477 608 ribonuclease HI, large subunit 4.87 up 0.00005<BR> rc\_AA262887\_at AA262887 610 EST 5.4 up 0.04719<BR> rc\_AA262943\_at AA262943 611 EST 13.42 up 0.00234<BR> rc\_AA262969\_f\_at AA262969 613 ferritin, heavy polypeptide 1 4.49 up 0.00013<BR> AA263044\_s\_at AA263044 615 H2A histone family, member Y 4.13 up 0.00024<BR> rc\_AA278817\_at AA278817 618 EST 4.22 up 0.00061<BR> rc\_AA278838\_s\_at AA278838 620 EST 3 up 0.02832<BR> rc\_AA279177\_at AA279177 624 lymphocyte antigen 75 6.05 up 0.01821<BR> rc\_AA279840\_at AA279840 632 titin-cap (telethonin) 5.58 up 0.01253<BR> rc\_AA280283\_s\_at AA280283 637 EST 4.99 up 0.02644<BR> rc\_AA280734\_i\_at AA280734 639 KIAA0618 gene product 9.64 up 0.00003<BR> rc\_AA280928\_at AA280928 642 EST 3.27 up 0.04625<BR> rc\_AA282149\_s\_at AA282149 654 huntingtin interacting protein-1-related 4.19 up 0.00091<BR> rc\_AA282247\_at AA282247 657 EST 8 up 0.00014<BR> rc\_AA283085\_s\_at AA283085 667 EST 4.93 up 0.00382<BR> rc\_AA284879\_at AA284879 679 EST 24.68 up 0.0001<BR> rc\_AA284945\_at AA284945 680 EST 5.98 up 0.00026<BR> rc\_AA287022\_s\_at AA287022 685 thymidine kinase 1, soluble 4.51 up 0.02582<BR> rc\_AA287347\_at AA287347 687 EST 5.47 up 0.00034 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA287393\_at AA287393 688 EST 5.68 up 0.00062<BR> rc\_AA290674\_s\_at AA290674 692 eukaryotic translation initiation factor 4E binding protein 1 11.59 up 0.00036<BR> rc\_AA291137\_at AA291137 694 EST 5.21 up 0.00685<BR> rc\_AA291139\_at AA291139 695 EST 8.69 up 0.04573<BR> rc\_AA291168\_at AA291168 696 EST 40.67 up 0.0065<BR> AA291456\_s\_at AA291456 700 EST 3.96 up 0.03633<BR> rc\_AA291659\_at AA291659 702 EST 3.83 up 0.1934<BR> rc\_AA292379\_at AA292379 708 EST 6.04 up 0.00568<BR> rc\_AA292659\_at AA292659 710 EST 3.48 up 0.00037<BR> rc\_AA292765\_at AA292765 712 ZW10 interactor 7.14 up 0.02623<BR> rc\_AA292788\_s\_at AA292788 714 EST 7.69 up 0.00967<BR> rc\_AA292931\_at AA292931 715 EST 3.97 up 0.00067<BR> rc\_AA293719\_at AA293719 720 EST 4.69 up 0.2181<BR> AA295819\_s\_at AA295819 722 EST 8 up 0.01793<BR> AA29786\_at AA29786 727 EST 4.65 up 0.02821<BR> AA306121\_at AA306121 729 EST 4.85 up 0.00381<BR> AA307748\_s\_at AA307748 730 EST 3.7 up 0.00001<BR> AA320369\_s\_at AA320369 735 chromosome 19 open reading frame 3 4.33 up 0.00554<BR> AA328993\_s\_at AA328993 738 EST 3.66 up 0.00146<BR> rc\_AA331393\_at AA331393 739 EST 16.73 up 0.00848<BR> rc\_AA335091\_at AA335091 740 EST 5.28 up 0.0009<BR> rc\_AA335191\_f\_at AA335191 741 creatine kinase, brain 47.35 up 0.00419<BR> rc\_AA338729\_at AA338729 743 EST 3.33 up 0.00046<BR> rc\_AA338889\_f\_at AA338889 745 actin related protein 2/3 complex, subunit 4 (20 KD) 10.77 up 0.03782<BR> AA364267\_at AA364267 762 EST 5.01 up 0.00255<BR> rc\_AA370163\_at AA370163 766 EST 3.34 up 0.00643<BR> rc\_AA372018\_at AA372018 768 EST 14.3 up 0.00178<BR> AA372630\_s\_at AA372630 769 differentially expressed in

hematopoietic lineages 25.49 up 0.01743<BR> AA384184\_s\_at AA384184 774 KFZP586B0519 protein 3.38 up 0.01209<BR> rc\_AA394121\_at AA394121 778 lamin receptor 1 (67kD, ribosomal protein SA) 23.78 u 0.00099 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA397906\_at AA397906 782 DKFZP4341216 protein 3.2 up 0.00138<BR> rc\_AA397916\_f\_at AA397916 784 EST 3.27 up 0.02895<BR> rc\_AA398205\_at AA398205 789 EST 4.17 up 0.00004<BR> rc\_AA398761\_s\_at AA398761 799 EST 3.43 up 0.0726<BR> rc\_AA398908\_at AA398908 801 EST 38.69 up 0.01089<BR> rc\_AA399226\_at AA399226 803 tight junction protein 3 (zona occludens 3) 3.59up 0.02002<BR> rc\_AA400271\_at AA400271 814 EST 3.51 up 0.00742<BR> rc\_AA401958\_at AA401958 832 EST 3.62 up 0.01232<BR> rc\_AA402495\_at AA402495 838 EST 4.91 up 0.00235<BR> AA402937\_at AA402937 843 EST 3.11 up 0.00182<BR> rc\_AA402968\_at AA402968 844 EST 3.1 up 0.00453<BR> rc\_AA403159\_at AA403159 845 Ste-20 related kinase 7.33 up 0.00187<BR> rc\_AA404338\_at AA404338 849 EST 01.9 up 0.00668<BR> rc\_AA405310\_at AA405310 856 EST 3.23 up 0.00138<BR> rc\_AA405460\_at AA405460 857 EST 4.02 up 0.03492<BR> rc\_AA405715\_at AA405715 862 hypothetical protien 4.68 up 0.00898<BR> rc\_AA405791\_at AA405791 864 EST 21.22 up 0<BR> rc\_AA406145\_f\_at AA406145 870 EST 6.71 up 0.00047<BR> rc\_AA406218\_at AA406218 872 EST 4.88 up 0.02194<BR> rc\_AA406385\_at AA406385 876 DKFZP564B0769 protien 3.21 up 0.00724<BR> rc\_AA406542\_at AA406542 878 EST 8.27 up 0.00724<BR> rc\_AA410469\_at AA410469 883 EST 6.3 up 0.00103<BR> rc\_AA410508\_at AA410508 885 EST 16.04 up 0.02635<BR> rc\_AA10962\_s\_at AA10962 887 peroxisome proliferative activated receptor, delta 3.45 up 0.04574<BR> rc\_AA410972\_at AA410972 888 EST 3.12 up 0.00023<BR> rc\_AA411502\_at AA411502 889 EST 16.42 up 0.00241<BR> rc\_AA411685\_at AA411685 890 EST 3.83 up 0.00417<BR> rc\_AA411813\_at AA411813 893 postmeiotic segregation increased 2-like 11 6.76 up 0.03499<BR> rc\_AA412301\_at AA412301 899 EST 4.57 up 0.00026<BR> rc\_AA412403\_at AA412403 900 EST 3.09 up 0.00047<BR> rc\_AA412405\_s\_at AA412405 901 EST 13.82 up 0.01021 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA412720\_at AA412720 905 EST 3.6 up 0.01396<BR> rc\_AA416963\_at AA416963 911 EST .69 up 0.03956<BR> rc\_AA416973\_at AA416973 913 EST 3.61 up 0.0091<BR> rc\_AA419217\_at AA419217 923 DKFZP586E1422 protein 6.77 up 0.00045<BR> rc\_AA421562\_at AA421562 934 anterior gradient 2 (Xenopus laevis) homolog 56.3 up 0.0041<BR> rc\_AA42163\_at AA42163 935 EST 3.05 up 0.00487<BR> rc\_AA422049\_at AA422049 937 EST 3.38 up 0.0067<BR> rc\_AA422086\_at AA422086 938 EST 10.71 up 0.03418<BR> rc\_AA422150\_at AA422150 939 cytochrome P540 family member predicted from ESTs 17.14 up 0.00108<BR> rc\_AA424029\_at AA424029 943 EST 8.68 up 0.00081<BR> rc\_AA424487\_at AA424487 945 EST 38.41 up 0.00002<BR> rc\_AA424881\_at AA424881 949 EST 6.3 up 0.00556<BR> rc\_AA425279\_at AA425279 951 quiescin Q66.15 up 0.00083<BR> rc\_AA425401\_at AA425401 954 serine/threonine kinase 24 (Ste20, yeast homolog) 3.22 up 0.00625<BR> rc\_AA425852\_s\_at AA425852 958 EST 7.78 up 0.00239<BR> rc\_AA425852\_i\_at AA425852 958 EST 4.8 up 0.03874<BR> rc\_AA426447\_at AA426447 965EST 4.23 up 0.0309<BR> rc\_AA426521\_at AA426521 967 Sjogren's syndrome nuclear autoantigen 1 3.47 up 0.01161<BR> rc\_AA427442\_at AA427442 971 guanine nucleotide regulatory facot 3.43 up 0.01547<BR> AA427468\_s\_at AA427468 973 claudin 4 84.43 up 0<BR> rc\_AA427636\_at AA427636 976 EST 19.23 up 0.00145<BR> rc\_AA427825\_at AA427825 981 EST 3.32 up 0.01615<BR> rc\_aa427925\_s\_at AA427925 982 EST 3.23 up 0.01806<BR> rc\_AA427946\_at AA427946 983 dynein, axonemal, light polypeptide 4 3.01 up 0.00001<BR> AA428172\_f\_at AA428172 986 Notch (Drosophila) homolog 3 9.53 up 0.02562<BR> rc\_AA428964\_at AA428964 993 kallikrein 10 21.83 up 0.02324<BR> rc\_AA429009\_at AA429009 994 srine protease inhibitor, Kunitz type 1 30.04 up 0.00001<BR> rc\_AA429470\_at AA429470 996 EST 3.67 up 0.00782<BR> rc\_AA429472\_at AA429472 997 DKFZP434P106 protein 8.27 up 0.00208<BR> rc\_AA429636\_at AA429636 1001 hexokinase 2 10.43 up 0.00597<BR> AA429825\_at AA429825 1003 DKFZP566B023 protein 6.63 up 0.00032 Table 6A Genes up regulated in metastatic tissue versus normal sample set

2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR>  
rc\_AA429890\_s\_at AA429890 1004 cisplatin resistance associated 12.51 up 0.00053<BR>  
rc\_AA430032\_at AA430032 1009 pituitary tumor-transforming 1 16.87 up 0.00659<BR>  
rc\_AA430048\_at AA430048 1012 KIAA0160 protein 6.27 up 0.00631<BR> rc\_AA430674\_at  
AA430674 1018 EST 15.11 up 0.00293<BR> rc\_AA431719\_at AA431719 1025 EST 4.25 up  
0.00015<BR> rc\_AA431776\_at AA431776 1027 EST 3.24 up 0.01814<BR> rc\_AA431873\_at  
AA431873 128 EST 4.03 up 0.00785<BR> rc\_AA432162\_at AA432162 1029 DKFZP586B2022  
protein 3.48 up 0.03851<BR> rc\_AA433930\_at AA433930 1032 chondroitin 4-sulfotransferase 7.68 up  
0.02445<BR> rc\_AA434418\_at AA434418 1036 KIAA1115 protein 5.12 up 0.00498<BR>  
rc\_AA435526\_s\_at AA435526 1037 transferrin receptor (p90, CD71) 3.69 up 0.00139<BR>  
rc\_AA435665\_at AA435665 1040 EST 8.66 up 0.00001<BR> rc\_AA436027\_at AA436027 1050 EST  
3.71 up 0.003676<BR> rc\_AA436473\_s\_at AA436473 1052 EST 3.03 up 0.00133<BR>  
c\_AA436616\_at AA436616 1056 EST 3.18 up 0.04402<BR> rc\_AA437368\_at AA437368 1063 EST  
3.75 up 0.01317<BR> rc\_AA437387\_s\_at AA437387 1064 EST 3.81 up 0.01478<BR>  
rc\_AA441911\_at AA441911 1066 EST 3.81 up 0.01478<BR> AA44205\_s\_at AA442054 1067  
phospholipase C, gamma 1 (formerly subtype 148) 16.89 up 0.00205<BR> rc\_AA442763\_at AA442763  
1072 cyclin B2 5.09 up 0.02168<BR> rc\_AA43271\_at AA43271 1073 KIAA0546 protein 3.6 up  
0.01228<BR> rc\_AA443316\_s\_at AA443316 1075 v-Ha-ras Harvey rat sarcoma viral oncogene  
homolog 4.13 u 0.01729<BR> rc\_AA443941\_at AA443941 1085 tumor suppressing subtransferable  
candidate 1 3.57 up 0.01685<BR> rc\_AA446949\_at AA446949 1096 EST 3.41 up 0.03411<BR>  
rc\_AA446968\_at AA446968 1097 EST 3.45 up 0.02232<BR> rc\_AA447118\_s\_at AA447118 1099  
EST 3.03 up 0.01702<BR> rc\_AA447683\_at AA447687 1104 EST 11.42 up 0.00362<BR>  
rc\_AA447732\_at AA447732 1105 EST 3.3 up 0.00591<BR> rc\_AA447991\_at AA447991 1112 EST  
4.99 up 0.00173<BR> rc\_aa449073\_s\_at AA449073 1117 EST 6.89 up 0.01445<BR> rc\_AA449122\_at  
AA449122 1119 EST 3.65 up 0.00369 Table 6A. Genes up regulated in metastatic tissue versus normal  
sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction  
Pvalue<BR> rc\_AA449456\_at AA449456 1126 EST 6.29 up 0.00087<BR> rc\_AA449456\_at  
AA449458 1127 EST 3.22 up 0.03098<BR> rc\_AA449475\_at AA449475 1128 EST 3.06 up  
0.00291<BR> rc\_AA449479\_at AA449479 1129 EST 3.09 up 0.03495<BR> rc\_AA450247\_at  
AA450247 1133 EST 5.27 up 0.02833<BR> rc\_AA451676\_at AA451676 1135 EST 14.72 up  
0.00056<BR> hepatocellular carcinoma associated proein; breast cancer<BR> rc\_AA451680\_at  
AA451680 1136 associated gene 1 3.55 up 0.00708<BR> rc\_AA451877\_at AA451877 1138 EST 8.63  
up 0.00489<BR> rc\_AA452259\_at AA452259 1143 EST 3.49 up 0.00114<BR> rc\_AA452536\_at  
AA452536 1145 v-ras similar leukemia viral oncogene homolog A (ras related) 5.6up 0.00481<BR>  
AA452724\_at AA452724 1149 programmed cell death 5 7.2 up 0.00908<BR> rc\_AA453477\_at  
AA453477 1153 X-prolyl aminopeptidase (aminopeptidase P)-like 4.23 up 0.0001<BR>  
rc\_AA453783\_s\_at AA453783 1158 EST 6.16 up 0.00167<BR> rc\_AA454597\_s\_at AA454597 1166  
EST 3.63 up 0.0067<BR> rc\_AA454710\_at AA454710 1168 EST 3.42 up 0.00653<BR>  
AA454908\_s\_at AA454908 1171 KIAA0144 gene product 9.3 up 0.00539<BR> rc\_AA455521\_s\_at  
AA455521 1178 E2F transcription factor 5, p130-binding 4.6 up 0.00773<BR> rc\_AA455522\_s\_at  
AA455522 1179 EST 3.83 up 0.00017<BR> rc\_aa458852\_f\_at AA458852 1203 KIAA0440 protein 3.2  
up 0.00038<BR> rc\_AA458890\_at AA458890 1206 EST 3.36 up 0.00303<BR> rc\_AA459254\_at  
AA459254 1211 EST 5.36 up 0.0259<BR> rc\_AA459310\_r\_at AA459310 1214 EST 3.45 up  
0.00179<BR> rc\_AA459388\_s\_at AA459388 1215 copine I 5.23 up 0.00691<BR> rc\_AA459703\_at  
AA459703 1222 v-myc avian myelocytomatosis viral oncogene homolog 4.75 up 0.02413<BR>  
rc\_AA459961\_at AA459961 1223 EST 3.24 up 0.00316<BR> rc\_AA460017\_i\_at AA460017 1225  
EST 10.76 up 0.00106<BR> rc\_AA460017\_f\_at AA460017 1225 EST 3.61 up 0.00109<BR>  
rc\_AA461187\_at AA461187 1236 EST 8.15 up 0.00068 Table 6A. Genes up regulated in metastatic  
tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change  
Direction Pvalue<BR> rc\_AA461473\_at AA461473 1242 nebulin 3.35 up 0.03855<BR>  
rc\_AA461476\_at AA461476 1243 ET 4.12 up 0.00871<BR> rc\_AA463234\_at AA463234 1246

KIAA0792 gene product 5.94 up 0.01182<BR> mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N<BR> rc\_AA463725\_at AA463725 1249 acetylglucosaminyltransferase 7.4 up 0.04715<BR> rc\_AA463861\_at AA463861 1251 EST 24.79 up 0.00096<BR> rc\_AA4614414\_i at AA464414 1258 EST 4.99 up 0.00529<BR> rc\_AA464698\_at AA464698 1262 EST 3.24 up 0.04854<BR> rc\_AA464963\_at AA464963 1265 EST 5.01 up 0.00107<BR> BUB3 (budding uninhibited by benzimidazoles 3, yeast)<BR> AA471278\_at AA471278 1277 homolog 5.14 up 0.00873<BR> rc\_AA476216\_at AA476216 1279 EST 4.97 up 0.00359<BR> rc\_AA478017\_at AA478017 1295 zyxin 6.15 up 0.01625<BR> rc\_AA478300\_at AA478300 1298 CD39-like 2 6.15 up 0.01625<BR> rc\_AA478415\_at AA478415 1299 EST 4.56 up 0.00095<BR> rc\_AA478599\_at AA478599 1304 G proteon-coupled receptor 56 3.31 up 0.00182<BR> rc\_AA479044\_s at Aa479044 1307 EST 6.9 up 0.04668<BR> rc\_AA479727\_s at AA479727 1315 EST 6.06 up 0.00389<BR> rc\_AA479797\_at AA479797 1316 EST 7.93 up 0.00006<BR> rc\_AA479945\_s at AA479945 1319 plakophilin 3 3.17 up 0.01767<BR> rc\_AA482007\_at AA48207 1331 EST 3.49 up 0.00167<BR> protein kinase related to S. cerevisiae STE20, effector for<BR> rc\_AA482127\_at AA482127 1333 Cdc42Hs 4.88 up 0.00017<BR> rc\_AA482224\_f at AA482224 1334 putative type II membrane protein 4.62 up 0.0105<BR> AA482319\_f at AA482319 1335 putative tye II membrane protein 5.11 up 0.00177<BR> rc\_AA482546\_s at AA482546 1336 KIAA0124 protein 4.41 up 0.00604<BR> rc\_AA482613\_at AA482613 1338 DKFZP434B203 protein 4.14 up 0.00186<BR> rc\_AA485405\_at AA485405 1343 EST 5.35 up 0.03475<BR> rc\_AA485697\_at AA485697 1346 EST 14.74 up 0.00102<BR> rc\_AA488987\_s at AA488987 1365 synaptogyrin 2 3.24 up 0.01444<BR> rc\_AA489707\_at AA489707 1371 EST 3.47 up 0.3433 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq Id Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA489712\_at AA489712 1372EST 4.93 up 0.00726<BR> rc\_AA490212\_at AA490212 1375 H2A histone family, member Y 3.71 up 0.01226<BR> rc\_AA490494\_at AA490494 1377 EST 5.16 up 0.01696<BR> rc\_AA491223\_at AA491223 1389 EST 3.03 up 0.00557<BR> rc\_AA496204\_at AA496204 1397 EST 3.69 up 0.01097<BR> rc\_AA496245\_at AA496245 1398 EST 3.96 up 0.0039<BR> v-erb-b2 avian erythroblastic leukemia viral oncogene homolog<BR> rc\_AA496981\_at AA496981 1404 3 4.93 up 0.01096<BR> rc\_AA497031\_at AA497031 1407 EST 11.05 up 0.04381<BR> rc\_AA504111\_at AA504111 1409 EST 3.81 up 0.00684<BR> rc\_AA504270\_at AA504270 1411 EST 4.96 up 0.01919<BR> AA504413\_at AA%04413 1413 EST 3.35 up 0.00079<BR> rc\_AA504806\_at AA504806 1416 EST 3.54 up 0.00221<BR> rc\_AA598405\_at AA598405 1424 membrane interacting protein of RGS16 4.69 up 0.0122<BR> rc\_AA498506\_s at AA598506 1430 KIAA0179 protein 3.17 up 0.01694<BR> rc\_AA598712 at AA598712 1436 EST 3.03 up 0.03656<BR> rc\_AA598988\_at AA598988 1442 EST 4.32 up 0.00044<BR> rc\_AA599244\_at AA599244 1448 KIAA0530 protein 3.39 up 0.01246<BR> rc\_AA599522\_f at AA599522 1452 squamous ell carcinoma antigen recognised by T cells 6.75 up 0.04229<BR> rc\_AA608579\_s at AA608579 1464 paired-like hmeodomain transcritpion factor 2 4.29 up 0.04435<BR> rc\_AA608897\_at AA608897 1473 EST 9.92 up 0.0087<BR> rc\_AA608965\_at AA608965 1474 Hemansky-Pudlak syndrome 3.19 up 0.00204<BR> rc\_AA609008\_at AA609008 1475 EST 3.46 up 0.02935<BR> rc\_AA609013\_s at AA609013 1477 dipeptidase 1 (renal) 10.17 up 0.00109<BR> rc\_AA606914\_at AA60964 1487 EST 6.5 up 0.00406<BR> rc\_AA609786\_s at AA6076 1491 nucleolar protein 1 (120kD) 4.75 up 0.00261<BR> rc\_AA610053\_at AA610053 1496 EST 7.01 up 0.00003<BR> rc\_AA61116\_i at AA610116 1499 tetraspan NEt-6 protein 33.68 up 0.00171<BR> rc\_AA620466\_at AA620466 1502 EST 5.14 up 0.00004 Table 6A. Genes up regulated in metastatic tissue versus normal sample set s.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fld Change Direction Pvalue<BR> rc\_AA620881\_at AA620881 1510 trinucleotide repeat containing 3 8.66 up 0.00735<BR> rc\_AA620995\_at AA620995 1512 EST 3.74 up 0.03414<BR> rc\_AA621277\_at AA621277 1520 EST 3.81 up 0.00194<BR> rc\_AA621780\_at AA621780 1530 CGI-96 protein 3.65 up 0.01582<BR> AB0005484\_at AB000584 1533 prostate differentiation fator 4.7 up 0.00071<BR> AB002533\_at AB002533 1539 karyopherin alpha 4 (importin alpha 3) 6.38 up 0.00003<BR> AB006781\_s at AB006781 1540 lectin, galactoside-binding, soluble, 4 (galectin 4) 7.05 up 0.00913<BR> AF001294\_at



AF001294 1544 tmor suppressing subtransferable candidate 3 7.45 up 0.00009<BR> AF003521\_at AF003521 15645 jagged 2 11.26 up 0.00008<BR> AF004709\_at AF004709 1547 mitogen-activated protein kinase 13 3.92 up 0.0009<BR> stress-associated endoplasmic reticulum protein 1; ribosome<BR> C00021\_s\_at C00021 1551 associated membrane protein 4 3.33 up 0.00215<BR> C01766\_s\_at C01766 1559 EST 13.67 up 0.00003<BR> rc\_C13992\_f\_at C13992 1564 EST 6.39 up 0.00059<BR> rc\_C14051\_f\_at C14051 1565 phosphoprotein enriched in astrocytes 15 3.68 up 0.01453<BR> rc\_C14098\_f\_at C14098 1566 EST 3.53 up 0.04401<BR> rc\_C14348\_at C14348 1568 EST 4.06 up 0.00111<BR> C14412\_s\_at C14412 1569 HSPC038 protein 3.9 up 0.00036<BR> rc\_C14756\_f\_at C14756 1570 MLN51 protein 5.36 up 0.00001<BR> rc\_C15324\_f\_at C15324 1574 EST 5.22 up 0.00344<BR> rc\_C21248\_at C21248 1585 pituitary tumor-transforming 1 3.85 up 0.00456<BR> D00017\_at D00017 1587 annexin A2 11.38 up 0<BR> interleukin 2 receptor, gamma (severe combined 0<BR> D11086\_at D11086 1595 immunodeficiency)<BR> heterogeneous nuclear ribonucleoprotein U (scaffold<BR> D13413\_ma1\_s\_at D13413 1604 attachment factor A) 4.79 up 0.00092<BR> D13639\_at D13639 1607 cyclin D2 7.49 up 0.01641<BR> D14520\_at D14520 1613 basic transcription element binding protein 2 4.93 up 0.00004<BR> D14530\_at D14530 1614 ribosomal protein S23 3.1 up 0.00331<BR> D14657\_at D14657 1615 KIAA0101 gene product 3.7 up 0.04079<BR> rc\_D19737\_at D19737 1623 golgi autoantigen, golgin subfamily a, 3 3.44 up 0.02212

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_D20464\_at D20464 1625 bromodomain adjacent to zinc finger domain, 2B 3.27 up 0.04897<BR> rc\_D20906\_at D20906 1627 EST 5.18 up 0.02189<BR> minichromosome maintenance deficient (S. cerevisiae) 2<BR> D21063\_at D21063 1628 (mitotin) 3.83 up 0.00983<BR> D21261\_at D21261 1629 transgelin 2 3.46 up 0.00685<BR> D23660\_at D23660 1630 ribosomal protein L4 3.22 up 0.00316<BR> D25216\_at D25216 1631 KIAA0014 gene product 3.17 up 0.02125<BR> D25274\_at D25274 1632 EST 3.39 up 0.00238<BR> D25328\_at D25328 1633 phosphofructokinase, platelet 3.17 up 0.04925<BR> rc\_D25560\_i\_at D25560 1634 EST 4.72 up 0.00661<BR> D26129\_at D26129 1635 ribonuclease, RNase A family, 1 (pancreatic) 5.68 up 0.03827<BR> neuroblastoma candidate region, suppression of tumorigenicity<BR> D28124\_at D28124 1636 1 6.38 up 0.00015<BR> D31094\_at D31094 1639 G8 protein 4.41 up 0.04845<BR> D31417\_at D31417 1645 secreted protein or unknown function 4.56 up 0.00014<BR> D38073\_at D38073 1651 minichromosome maintenance deficient (S. cerevisiae) 3 3.65 up 0.01869<BR> D38548\_at D38548 1655 KIAA0076 gene product 4.5 up 0.00036<BR> D38583\_at D38583 1656 S100 calcium-binding protein A11 (calgizzarin) 18.7 up 0.00003<BR> D42085\_at D42085 1658 KIAA0095 gene product 3.83 up 0.00036<BR> D43949\_at D43949 1659 KIAA0082 protein 3.32 up 0.0014<BR> D43950\_at D43950 1660 chaperonin containing TCP1, subunit 5 (epsilon) 3.61 up 0.00672<BR> D49400\_at D49400 1667 ATPase, vacuolar, 14 kD 4.01 up 0.00287<BR> D50663\_at D50663 1671 t-complex-associated-testis-expressed 1-like 1 4.09 up 0.00208<BR> D50913\_at D50913 1672 KIAA0123 protein 3.32 up 0.01202<BR> D50914\_at D50914 1673 KIAA0124 protein 4.74 up 0.00752<BR> rc\_D51112\_s\_at D51112 1675 collapsin response mediator protein 1 10.48 up 0.00076<BR> rc\_D51133\_f\_at D51133 1676 tubulin, beta, 4 4.84 up 0.02875<BR> rc\_D51276\_f\_at D51276 1678 leukemia-associated phosphoprotein p18 (stathmin) 4.81 up 0.00514<BR> rc\_D51287\_f\_at D51287 1680 ribosomal protein S12 3.3 up 0.02829<BR> rc\_D51393\_f\_at D51393 1681 ribosomal protein L4 5.64 up 0.00074

Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_D52632\_f\_at D52632 1683 ribosomal protein S6 3.12 up 0.00498<BR> rc\_D53139\_f\_at D53139 1684 ribosomal protein S28 4.38 up 0.0009<BR> rc\_D54296\_f\_at D54296 1685 KIAA0255 gene product 3.8 up 0.01059<BR> D55716\_at D55716 1686 minichromosome maintenance deficient (S. cerevisiae) 7 6.6 up 0.00151<BR> rc\_D57489\_at D57489 1689 chaperonin containing TCP1, subunit 7 (eta) 4.08 up 0.00001<BR> rc\_D59322\_f\_at D59322 1694 EST 4.18 up 0.00006<BR> rc\_D59847\_at D59847 1701 EST 3.09 up 0.02206<BR> rc\_D60811\_s\_at D60811 1704 eST 3.22 up 0.0098<BR> platelet-activating factor acetylhydrolase, isoform Ib, gamma<BR> D63391\_at D63391 1710 subunit (29kD) 3.91 up 0.00062<BR> D63486\_at D63486 1712

KIAA0152 gene product 6.33 up 0.00078<BR> D63487\_at D63487 1713 KIAA0153 protein 5.4 up 0.00027<BR> D63874\_at D63874 1714 high-mobility group (nonhistone chromosomal) protein 1 3.64 up 0.00228<BR> D63880\_at d63880 1715 KIAA0159 gene product 4.26 up 0.00253<BR> D78361\_at D78361 1718 EST 3.14 up 0.00023<BR> D78676\_at D78676 1719 EST 3.2 up 0.00635<BR> D79205\_at D79205 1721 ribosomal protein L39 3.07 up 0.00021<BR> rc\_D80237\_s\_at D80237 1729 actin related protein 2/3 complex, subunit 4 (20 kD) 3.27 up 0.00137<BR> rc\_D80662\_s\_at D80662 1733 adaptor-related protein complex 1, gamma 2 subunit 3.43 up 0.100108<BR> rc\_D80710\_f\_at D80710 1734 integral type I protein 7.08 up 0.00213<BR> rc\_D80917\_f\_at D80917 1736 KIAA0670 protein/acinus 3.58 up 0.00007<BR> rc\_D80946\_f\_at D80946 1737 SFRS protein kinase 1 8.53 up 0.00455<BR> 5-aminoimidazole-4-carboxamide ribonucleotide<BR> D82348\_at D82348 1744 formyltransferase/IMP cyclohydrolase 3.93 up 0.00037<BR> D82558\_at D82558 1746 novel centrosomal protein RanBPM 5.94 up 0.00752<BR> D83735\_at D83735 1747 calponin 2 10.42 up 0.00001<BR> trinucleotide repeat containing 11 (THR-associated protein, 230<BR> D83783\_at D83783 1748 kDa subunit) 6.55 up 0.00176 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbak Seq ID Known Gene Name Fold Change Direction Pvalue<BR> trinucleotide repeat containing 11 (THR-associated protein, 230<BR> D83783\_at D83783 1748 kDa subunit) 3.33 up 0.00748<BR> D86956\_at D86956 1753 heat shock 105kD 4 up 0.03013<BR> D86974\_at D86974 1756 KIAA0220 protein 3.85 up 0.0161<BR> D87735\_at D87735 1764 ribosomal protein L14 3.92 up 0.00015<BR> D87953\_at D87953 1765 N-myc downstream regulated 6.12 up 0.00033<BR> D88154\_at D88154 1766 villin-like 4.18 up 0.00051<BR> rc\_F01444\_f\_at F01444 1770 KIAA0440 protein 6.78 up 0.00028<BR> rc\_F01568\_at F01568 1772 EST 3.24 up 0.0018<BR> rc\_F02800\_at F02800 1780 EST 3.45 up 0.03238<BR> rc\_F02863\_at F02863 1782 EST 3.21 up 0.01039<BR> rc\_F04320\_s\_at F04320 1786 replication factor C (activator 1) 4 (37kD) 3.63 up 0.01119<BR> rc\_F04444\_at F04444 1788 EST 4.57 up 0.01132<BR> rc\_F04531\_s\_at F04531 1791 Kell blood group precursor (McLeod phenotype) 7.79 up 0.03205<BR> rc\_F04674\_at F04674 1793 KIAA0746 protein 8.2 up 0.00028<BR> rc\_F09297\_s\_at F09297 1800 EST 3.94 up 0.0016<BR> rc\_F09394\_s\_at F09394 1803 KIAA0715 protein 22.89 up 0.01753<BR> rc\_F09684at F09684 1805 EST 3.78 up 0.00277<BR> procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-<BR> rc\_F09788\_at F09788 1808 hydroxylase), alpha polypeptide II 4.14 up 0.00003<BR> rc\_F13809\_f\_at F13809 1828 tropomyosin 1 (alpha) 7.62 up 0.00012<BR> rc\_H04753\_f\_at H04753 1839 EST 3.38 up 0.02447<BR> rc\_H04799\_at H04799 1841 EST 3.71 up 0.04109<BR> rc\_H05394\_f\_at H05394 1845 KIAA0266 gene product 4.06 up 0.0015<BR> rc\_H05525\_s\_at H05525 1846 hypothetical protein 4.6 up 0.0033<BR> rc\_H05625\_f\_at H05625 1847 EST 5.17 up 0.04551<BR> rc\_H08863\_at H08863 1859 hypothetical protein 3.48 up 0.00205<BR> rc\_H09241\_s\_at H09241 1861 EST 4.17 up 0.00727<BR> rc\_H09271\_f\_at H09271 1862 EST 5.06 up 0.0016<BR> rc\_H09281\_at H09281 1863 EST 6 up 0.00966<BR> rc\_H13532\_f\_at H13532 1881 ribosomal protein L18a 3.97 up 0.00061 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_H17476\_at H17476 1889 EST 3.44 up 0.00479<BR> rc\_H18412\_s\_at H18412 1890 isocitrate dehydrogenase 3 (NAD+) gamma 4.37 up 0.00262<BR> rc\_H18442\_f\_at H18442 1891 creatine kinase, brain 17.42 up 0.02391<BR> rc\_H20989\_s\_at H20989 1899 pyruvate kinase, muscle 11.37 up 0.0375<BR> rc\_H24077\_at H24077 1900 EST 3.05 up 0.0324<BR> rc\_H27188\_f\_at H27188 1908 collagen-binding protein 2 (colligen 2) 4.16 up 0.02073<BR> rc\_H28333\_f\_at H28333 1912 melanoma adhesion molecule 3.11 up 0.00172<BR> rc\_H29565\_at H29565 1913 EST 3.89 up 0.01856<BR> rc\_H38240\_s\_at H38240 1916 thrombospondin 2 4.28 up 0.0066<BR> rc\_H38568\_s\_at H38568 1918 EST 4.86 up 0.0003<BR> rc\_H42321\_f\_at H42321 1928 ribosomal protein L18a 3.23 up 0.01102<BR> H43286\_s\_at H43286 1929 gamma-aminobutyric acid (GABA) B receptor, 1 5.02 up 0.01972<BR> rc\_H43646\_at H43646 1930 H2A histone family, member Y 4.6 up 0.00147<BR> H46486\_s\_at H46486 1932 nesca protein 4.77 up 0.00421<BR> rc\_H49637\_s\_at H49637 1940 EST 3.79 up 0.01092<BR> rc\_H52673\_s\_at H52673 1943 BLC2-antagonist/killer 1 3.03 up 0.0393<BR> H53657\_s\_at H53657 1945 adenylate cyclase 3 3.98 up 0.0045<BR> H55437\_at H55437 1948 kraken-



like 3.53 up 0.02344<BR> rc\_H56345\_r\_at H56345 1950 EST 4.15 up 0.00488<BR> solute carrier family 2 (facilitated glucose transporter), member<BR> rc\_H58873\_s\_at H58873 1961 1 57.98 up 0.00063<BR> rc\_H59617\_at H59617 1964 EST 3.3 up 0.04588<BR> rc\_H75933\_f\_at H75933 1998 laminin receptor 1 (67kD, ribosomal protein SA) 5.81 up 0.00024<BR> rc\_H78211\_at H78211 2001 EST 6.73 up 0.02488<BR> rc\_H78323\_at H78323 2002 transcription factor Dp-1 3.69 up 0.00326<BR> high-mobility group (nonhistone chromosomal) protein isoforms<BR> rc\_H81413\_f\_at H81413 2007 I and Y 5.82 up 0.00769<BR> rc\_H88674\_s\_at H88674 2021 collagen, type 1, alpha 2 5.06 up 0.00866<BR> H89551\_s\_at H89551 2024 EST 9.94 up 0.00137<BR> rc\_H93021\_at H93021 2033 peptidylprolyl isomerase A (cyclophilin A) 3.31 up 0.0183<BR> rc\_H93492\_at H93492 2037 EST 3.94 up 0.01136 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_H93652\_f\_at H93652 2039 ribosomal protein S5 3.31 up 0.00788<BR> rc\_H94471\_at H94471 2042 occludin 43.09 up 0<BR> rc\_H95233\_s\_at H95233 2048 serine protease inhibitor, Kunitz type, 2 47.06 up 0<BR> rc\_H96975\_at H96975 2057 EST 3.22 up 0.0141<BR> rc\_H97013\_at H97013 2059 ephrin-A4 9.14 up 0.00346<BR> rc\_H97809\_at H97809 2063 EST 4.05 up 0.00111<BR> rc\_H98924\_at H93924 2072 chromatin assembly factor 1, subunit A (p150) 3.53 up 0.02106<BR> rc\_H99473\_s\_at H99473 2077 regulator of nonsense transcripts 1 5.37 up 0.00177 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> J03459\_at J03459 2093 leukotriene A4 hydrolase 3.03 up 0.04041<BR> J03464\_s\_at J03464 2094 collagen, type 1, alpha 2 9.81 up 0.00028<BR> solute carrier family 25 (mitochondrial carrier; adenine<BR> J03592\_at J03592 2096 nucleotide translocator), member 6 10.05 up 0<BR> J03827\_at J03827 2100 nuclease sensitive element binding protein 1 4.45 up 0.00015<BR> membrane component, chromosome 1, surface marker 1<BR> J04152\_ma1\_s\_at J04152 2107 (40kD glycoprotein, identified by monoclonal antibody GA733) 5.26 up 0.02466<BR> J04164\_at J04164 2108 interferon induced transmembrane protein 1 (9-27) 12.37 up 0.00001<BR> AFFX-BioDn-3\_at J04423 2109 EST 54.11 up 0.02774<BR> AFFX-BioDn-3\_at J04423 2109 EST 48.05 up 0.02203<BR> AFFX-BioDn-3\_at J04423 2109 EST 21.46 up 0.04283<BR> AFFX-BioB-3\_at J04423 2109 EST 5.13 up 0.02791<BR> AFFX-BioB-5\_at J04423 2109 EST 4.47 up 0.02754<BR> AFFX-BioDn-3\_st J04423 2109 EST 4.35 up 0.01245<BR> J04469\_at J04469 2111 creatine kinase, mitochondrial 1 (ubiquitous) 7.9 up 0.00705<BR> J04823\_ma1\_at J04823 2115 cytochrome c oxidase subunit VIII 3.35 up 0.00075<BR> J05257\_at J05257 2118 dipeptidase 1 (renal) 12.02 up 0.02099<BR> J05582\_s\_at J05582 2121 mucin 1, transmembrane 5.39 up 0.00056<BR> solute carrier family 2 (facilitated glucose transporter), member<BR> K03195\_at K03195 2128 1 10.73 up 0.00139<BR> K03460\_at K03460 2129 tubulin, alpha 1 (testis specific) 7.5 up 0.00002<BR> L03411\_s\_at L03411 2134 RD RNA-binding protein 3.97 up 0.00422<BR> L04483\_s\_at L04483 2136 ribosomal protein S21 4.2 up 0.00057<BR> NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9<BR> L04490\_at L04490 2137 (39kD) 5.22 up 0.02192 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> L06499\_at L06499 2141 ribosomal protein L37a 4.34 up 0.01103<BR> L06505\_at L06505 2142 ribosomal protein L12 5 up 0.00163<BR> L08044\_s\_at L08044 2149 trefoil factor 3 (intestinal) 21.42 up 0.01674<BR> L08044\_s\_at L08044 2149 trefoil factor 3 (intestinal) 14.18 up 0.02124<BR> L09604\_at L09604 2151 proteolipid protein 2 (colonic epithelium-enriched) 8.68 up 0<BR> L11566\_at L11566 2156 ribosomal protein L18 4.29 up 0.00014<BR> L11669\_at L11669 2157 tetracycline transporter-like protein 6.75 up 0.00101<BR> L12350\_at L12350 2160 thrombospondin 2 3.78 up 0.00061<BR> L12711\_s\_at L12711 2161 transketolase (Wernicke-Korsakoff syndrome) 3.08 up 0.03362<BR> high-mobility group (nonhistone chromosomal) protein isoforms<BR> L17131\_ma1\_at L17131 2168 I and Y 20.57 up 0.00058<BR> L19527\_at L19527 2169 ribosomal protein L27 3.54 up 0.00025<BR> L19605\_at L19605 2170 annexin A11 6.38 up 0.00017<BR> macrophage migration inhibitory factor (glycosylation-inhibiting<BR> L19686\_ma1\_at L19686 2171 factor) 5.26 up 0.00562<BR> L20591\_at L20591 2173 annexin A3 4.64 up 0.00065<BR> L20941\_at L20941 2174 ferritin, heavy polypeptide 1 3.3 up 0.01172<BR> L21954\_at L21954 2177 benzodiazapine receptor

(peripheral) 8.53 up 0.00001<BR> L23808\_at L23808 2179 matrix metalloproteinase 12 (macrophage elastase) 6.18 up 0.02195<BR> L25081\_at L25081 2180 ras homolog gene family, member C 3.67 up 0.00005<BR> L33075\_at L33075 2195 IQ motif containing GTPase activating protein 1 3.83 up 0.00015<BR> L33842\_rna1\_at L33842 2197 IMP (inosine monophosphate) dehydrogenase 2 11.03 up 0.00001<BR> L33930\_s\_at L33930 2198 CD24 antigen (small cell lung carcinoma cluster 4 antigen) 9.16 up 0.01252<BR> transcription elongation factor B (SIII), polypeptide 1 (15kD,<BR> L34587\_at L34587 2200 elongin C) 4.32 up 0.00287<BR> L36720\_at L36720 2205 bystin-like 3.46 up 0.00094<BR> L38696\_at L38696 2208 RNA-binding protein (autoantigenic) 3.7 up 0.00093<BR> thyroid receptor interacting protein 10 (CDC42-interacting<BR> L40379\_at L40379 2210 protein) 3.87 up 0.00207<BR> L40904\_at L40904 2212 peroxisome proliferative activated receptor, gamma 3.43 up 0.03511 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> L41351\_at L41351 2214 protease, serine, 8 (prostasin) 6.34 up 0.01132<BR> L44538\_at L44538 2217 EST 4.34 up 0.04319<BR> L76191\_at L76191 2222 interleukin-1 receptor-associated kinase 1 5.66 up 0.00089<BR> L76200\_at L76200 2223 guanylate kinase 1 3.24 up 0.0097<BR> AFFX-HUMRGE/M10098M10098 2231 EST 11.55 UP 0.00099<BR> AFFX-HUMRGE/M10098M10098 2231 EST 10.2 UP 0.00027<BR> AFFX-HUMRGE/M10098M10098 2231 EST 5.62 UP 0.00251<BR> AFFX-HUMRGE/M10098M10098 2231 EST 5.61 UP 0.01238<BR> AFFX-HUMRGE/M10098M10098 2231 EST 5.35 UP 0.00186<BR> AFFX-HUMRGE/M10098M10098 2231 EST 4.79 UP 0.00328<BR> AFFX-HUMRGE/M10098M10098 2231 EST 4.66 UP 0.00405<BR> AFFX-HUMRGE/M10098M10098 2231 EST 3.73 UP 0.01794<BR> M12125\_at M12125 2241 tropomyosin 2 (beta) 10.83 up 0.00191<BR> M13934\_cds2\_at M13934 2255 ribosomal protein S14 3.99 up 0<BR> M14199\_s\_at M14199 2258 laminin receptor 1 (67kD, ribosomal protein SA) 7.01 up 0<BR> M14483\_rna1\_s\_at M14483 2261 prothymosin, alpha (gene sequence 28) 4.46 up 0.00686<BR> M14949\_at M14949 2264 related RAS viral (r-ras) oncogene homolog 3.11 up 0.00013<BR> M15205\_at M15205 2265 thymidine kinase 1, soluble 3.75 up 0.00159<BR> M16364\_s\_at M16364 2269 creatine kinase, brain 12.69 up 0.03633<BR> M17733\_at M17733 2280 thymosin, beta 4, X chromosome r.15 up 0.00009<BR> M17885\_at M17885 2281 ribosomal protein, large, P0 3.92 up 0.00003<BR> M17886\_at M17886 2282 ribosomal protein, large, P1 4.34 up 0.00004<BR> M18000\_at M18000 2283 ribosomal protein S17 3.79 up 0.00004<BR> carcinoembryonic antigen-related cell adhesion molecule 6 (non<BR> M18728\_at M18728 2285 specific cross reacting antigen) 44.82 up 0.00291<BR> M20471\_at M20471 2289 clathrin, light polypeptide (Lca) 5.32 up 0.00344<BR> M22960\_at M22960 2296 protective protein for beta-galactosidase (galactosialidosis) 4.49 up 0.00898<BR> M23613\_at M23613 2301 nucleophosmin (nucleolar phosphoprotein B23, numatrin) 3.67 up 0.00977 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> guanine nucleotide binding protein (G protein), beta polypeptide<BR> M24194\_at M24194 2302 2-like 1 4.55 up 0.00017<BR> M24485\_s\_at M24485 2304 glutathione S-transferase pi 10.2 up 0.00003<BR> M26708\_s\_at M26708 2311 prothymosin, alpha (gene sequence 28) 3.35 up 0.00064<BR> M27826\_at M27826 2313 endogenous retroviral protease 26.36 up 0.00342<BR> AFFX-M27830\_5\_at M27830 2314 EST 15.53 up 0.00022<BR> AFFX-M27830\_5\_at M27830 2314 EST 14.86 UP 0.00043<BR> AFFX-M27830\_5\_at M27830 2314 EST 10.64 UP 0.00213<BR> AFFX-M27830\_M\_at M27830 2314 EST 9.8 UP 0.00041<BR> AFFX-M27830\_M\_at M27830 2314 EST 8.78 UP 0.00003<BR> AFFX-M27830\_5\_at M27830 2314 EST 8.2 UP 0.00294<BR> AFFX-M27830\_M\_at M27830 2314 EST 6.25 UP 0.00046<BR> AFFX-M27830\_M\_at M27830 2314 EST 5.78 UP 0.0017<BR> M29277\_at M29277 2316 melanoma adhesion molecule 3.91 up 0.00112<BR> M29540\_at M29540 2317 carcinoembryonic antigen-related cell adhesion molecule 5 36.57 up 0.0116<BR> M30496\_at M30496 2324 ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) 3.8 up 0.00478<BR> M31303\_rna1\_at M31303 2327 leukemia-associated phosphoprotein p18 (stathmin) 7.48 up 0.00021<BR> M31520\_rna1\_s\_at M31520 2328 ribosomal protein S24 3.37 up 0.00077<BR> M31520\_at M31520 2328 ribosomal protein S24 3.13 up 0.00014<BR> M32405\_at

M32405 2334 ribosomal protein S15 4.01 up 0.00055<BR> M32886\_at M32886 2335 sorcin 8.35 up 0.00215<BR> AFFX-HUMGAPDH/M33 M33197 2337 glyceraldehyde-3-phosphate dehydrogenase 3.31 up 0.00009<BR> M34182\_at M34182 2340 protein kinase, cAMP-dependent, catalytic, gamma 4.51 up 0.00043<BR> M35252\_at M35252 2343 transmembrane 4 superfamily member 3 39.12 up 0<BR> M36072\_at M36072 2347 ribosomal protein L7a 3.1 up 0.00006<BR> S100 calcium-binding protein A10 (annexin II ligand, calpactin I,<BR> M38591\_at M38591 2350 light polypeptide (p11) 14.87 up 0<BR> M38690\_at M38690 2351 CD9 antigen (p24) 9.08 up 0.00059<BR> M55998\_s\_at M55998 2356 collagen, type I, alpha 1 6.99 up 0.00103 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> M57710\_at M57710 2357 lectin, galactoside-binding, soluble, 3 (galectin 3) 27.12 up 0.00001<BR> M60784\_s\_at M60784 2366 small nuclear ribonucleoprotein polypeptide A 5.74 up 0.00126<BR> M60854\_at M60854 2367 ribosomal protein S16 3.4 up 0.00001<BR> M62895\_s\_at M62895 2375 annexin A2, annexin A2 pseudogene 2 6.11 up 0.00013<BR> M64716\_at M64716 2382 ribosomal protein S25 3.16 up 0.00039<BR> M68864\_at M68864 2389 ORF 3.1 up 0.00603<BR> M77232\_ma1\_at M77232 2399 ribosomal protein S6 3.82 up 0.00045<BR> M77349\_at M77349 2400 transforming growth factor, beta-induced, 68kD 4.81 up 0.00546<BR> M77836\_at M77836 2401 pyrroline-5-carboxylate reductase 1 3.43 up 0.00759<BR> M79463\_s\_at M79463 2402 promyelocytic leukemia 4.88 up 0.01821<BR> M81757\_at M81757 2406 ribosomal protein S19 5.46 up 0<BR> tyrosine 3-monooxygenase/tryptophan 5-monooxygenase<BR> M86400\_at M86400 2410 activation protein, zeta polypeptide 5.62 up 0.00016<BR> M86667\_at M86667 2411 nucleosome assembly protein 1-like 1 3.03 up 0.04853<BR> stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing<BR> M86752\_at M86752 2412 protein) 7.32 up 0.00001<BR> M87339\_at M87339 2415 replication factor c (activator 1) 4 (37kD) 4.07 up 0.00316<BR> M91083\_at M91083 2419 chromosome 11 open reading frame 13 3.3 up 0.00163<BR> membrane component, chromosomal 4, surface marker (35kD<BR> M93036\_at M93036 2422 glycoprotein) 16.45 up 0.00308<BR> M94250\_at M94250 2426 midkine (neurite growth-promoting factor 2) 10.39 up 0.01818<BR> M94345\_at M94345 2427 capping protein (actin filament), gelsolin-like 22.38 up 0.00003<BR> M96739\_at M96739 2434 nescient helix loop helix 1 3.72 up 0.00015<BR> rc\_N20198\_s\_at N20198 2440 ubiquitin-conjugating enzyme E2 variant 1 5.17 up 0.00508<BR> rc\_N21359\_at N21359 2442 ESWT 4.43 up 0.00078<BR> rc\_N22015\_at N22015 2448 EST 46.61 up 0.00025<BR> rc\_N22107\_at N22107 2449 EST 6.88 up 0.04259<BR> rc\_N24899\_at N24899 2461 EST 3.06 up 0.00353<BR> rc\_N26186\_at N26186 2468 EST 6.15 up 0.00135<BR> rc\_N27186\_at N27186 2470 EST 3.79 up 0.00112<BR> rc\_N27334\_at N27334 2471 EST 3.65 up 0.03437 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_N29888\_at N29888 2483 EST 3.7 up 0.00226<BR> rc\_N30436\_f\_at N30436 2484 EST 3.45 up 0.02356<BR> rc\_N31570\_at N31570 2486 TNF receptor-associated factor 5 10.39 up 0.00018<BR> rc\_N31597\_s\_at N31597 2487 DKFZP564G2022 protein 4.44 up 0.00085<BR> N36432\_at N36432 2507 erythrocyte membrane protein band 4.1-like 2 3.03 up 0.03086<BR> rc\_N39099\_at N39099 2508 EST 4.42 up 0.00643<BR> rc\_N39237\_at N39237 2511 EST 9.29 up 0.00001<BR> rc\_N39254\_s\_at N39254 2512 EST 4.24 up 0.00478<BR> rc\_N46423\_at N46234 2521 EST 9.64 up 0.00027<BR> eukaryotic translation initiation factor 3, subunit 3 (gamma,<BR> rc\_N47956\_at N47956 2524 40kD) 6.34 up 0.00251<BR> rc\_N49284\_s\_at N49284 2537 v-myb avian myeloblastosis viral oncogene homolog 11.82 up 0.01981<BR> rc\_N49738\_at N49738 2539 EST 3.81 up 0.02479<BR> rc\_N50048\_at N50048 2542 EST 4.08 up 0.00085<BR> rc\_N51053\_s\_at N51053 2543 eukaryotic translation initiation factor 5 3.42 up 0.01326<BR> rc\_N51342\_at N51342 2545 EST 3.56 up 0.0001<BR> rc\_N52168\_at N52168 2551 EST 5.65 up 0.00003<BR> rc\_N54841\_at N54841 2572 EST 42.96 up 0.00002<BR> rc\_N56935\_s\_at N56935 2575 EST 3.57 up 0.00282<BR> rc\_N58463\_at N58463 2580 PCTAIRE protein kinase 1 3.18 up 0.00649<BR> rc\_N62126\_at N62126 2589 EST 8.51 up 0.00016<BR> rc\_N62675\_s\_at N62675 2594 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 3.61 up 0.04034<BR> rc\_N62819\_at N62819 2595 EST 3.25 up 0.01137<BR> rc\_N64616\_at N64616 2611 EST 3.11 up 0.0074<BR> rc\_N66139\_s\_at N66139 2615 neurochondrin

4.03 up 0.00118<BR> homolog of mouse quaking QKI (KHdomain RNA binding<BR> rc\_N66624\_at N66624 2618 protein) 6.25 up 0<BR> rc\_N66951\_at N66951 2621 EST 5.54 up 0.02442<BR> rc\_N67205\_at N67205 2625 EST 3.1 up 0.00626<BR> rc\_N68038\_f\_at N68038 2632 phorbolin (similar to apolipoprotein B mRNA editing protein) 3.75 up 0.01041 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_N68385\_f\_at N68385 2635 ribosomal protein L13a 3.57 up 0.00417<BR> rc\_N68921\_at N68921 2639 EST 4.4 up 0.00989<BR> rc\_N69252\_f\_at N69252 2647 ferritin, light polypeptide 5.33 up 0.01554<BR> rc\_N69263\_at N69263 2648 EST 7.47 up 0.00004<BR> rc\_N70577\_at N70577 2659 EST 3.07 up 0.01975<BR> rc\_N70678\_s\_at N70678 2660 TAR (HIV) RNA-binding protein 1 4.2 up 0.00119<BR> rc\_N70903\_at N70903 2662 EST 4.41 up 0.0078<BR> rc\_N71072\_at N71072 2662 EST 5.57 up 0.03881<BR> rc\_N71781\_at N71781 2666 EST 7.01 up 0.02952<BR> solute carrier family 11 (proton-coupled divalent metal ion<BR> rc\_N72116\_s\_at N72116 2668 transporter, member 2 9.01 up 0.00051<BR> rc\_N73762\_f\_at N73762 2678 EST 6.65 up 0.0023<BR> rc\_N73808\_f\_at N73808 2679 EST 8.46 up 0.01886<BR> rc\_N73846\_at N73846 2680 EST 3.27 up 0.00012<BR> rc\_N77947\_s\_at N77947 2698 EST 5 up 0.00117<BR> rc\_N80703\_at N80703 2704 EST 6.06 up 0.00003<BR> rc\_N89670\_at N89670 2709 EST 4.26 up 0.00002<BR> rc\_N89937\_at N89937 2711 LIM domain only 7 3.6 up 0.00375<BR> rc\_N90238\_i\_at N90238 2712 EST 3.06 up 0.00354<BR> rc\_N91023\_at N91023 2716 EST 3.87 up 0.00008<BR> amyloid beta (A4) precursor protein-binding, family A, member<BR> rc\_N92775\_at N92775 2723 3 (X11-like 2) 3.86 up 0.00577<BR> rc\_N92915\_at N92915 2724 brefeldin A-inhibited guanine nucleotide-exchange protein 1 3.1 up 0.00807<BR> rc\_N92934\_s\_at N92934 2725 cysteine-rich protein 1 (intestinal) 35.52 up 0.002<BR> rc\_N93105\_f\_at N93105 2728 EST 3.77 up 0.02195<BR> rc\_N93798\_at N93798 2738 protein tyrosine phosphatase type IVA, member 3 4.65 up 0.00118<BR> rc\_N98464\_s\_at N98464 2744 EST 15.5 up 0.00004<BR> rc\_N98758\_f\_at N98758 2745 EST 3.87 up 0.0074<BR> rc\_N99505\_at N99505 2746 EST 3.6 up 0.4499<BR> rc\_R02036\_at R02036 2754 EST 8.01 up 0.01012 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_R06251\_f\_at R06251 2764 tumor protein D52-like 2 5.57 up 0.00037<BR> rc\_R06254\_f\_at R06254 2765 tumor protein D52-like 2 4.64 up 0.00039<BR> rc\_R06866\_s\_at R06866 2774 EST 5.18 up 0.00187<BR> rc\_R06986\_f\_at R06986 2776 peptidylprolyl isomerase B (cylophilin B) 3.01 up 0.04418<BR> rc\_R22565\_at R22565 2800 EST 4.8 up 0.0424<BR> rc\_R26706\_s\_at R26706 2803 EST 3.21 up 0.03858<BR> rc\_R26744\_at R26744 2804 midline 1 (Opitz/BBB syndrome) 4.32 up 0.00532<BR> rc\_R27432\_at R27432 2808 EST 3.62 up 0.00014<BR> UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase,<BR> rc\_R28636\_at R28636 2809 polypeptide 3 3.78 up 0.00765<BR> rc\_R31107\_at R31107 2812 EST 4.12 up 0.00003<BR> rc\_R33498\_s\_at R33498 2820 EST 41.34 up 1.00001<BR> rc\_R36947\_s\_at R36947 2825 calcium channel, voltage-dependent, beta 3 subunit 4.11 up 0.00006<BR> rc\_r38076\_s\_at R38076 2828 EST 4.08 up 0.00374<BR> rc\_R38239\_at R38239 2830 EST 7.14 up 0.00249<BR> rc\_R38280\_at R38280 2831 BCS1 (yeast homolog)-like 3.68 up 0.0009<BR> rc\_R38511\_s\_at R38511 2832 protein similar to E.coli yhdg and R. capsulatus nifR3 5.19 up 0.00015<BR> rc\_R39119\_s\_at R39119 2834 KIAA1020 protein 4.69 up 0.00456<BR> rc\_R40254\_at R40254 2840 EST 5.82 up 0.00304<BR> rc\_R43952\_at R43952 2853 homeo box B5 4.11 up 0.04316<BR> rc\_R44479\_at R44479 2855 KIAA0552 gene product 4.14 up 0.0181<BR> rc\_R44538\_at R44538 2856 EST 5.73 up 0.01015<BR> rc\_r45698\_at R45698 2866 EST 3.01 up 0.04766<BR> rc\_R45994\_f\_at R45994 2867 EST 7.81 up 0.0018<BR> rc\_R48447\_at R48447 2871 EST 7.75 up 0.00049<BR> rc\_R48589\_at R48589 2874 EST 4.95 up 0.01346<BR> rc\_R49084\_s\_at R49084 2879 KIAA0770 protein 3.57 up 0.00447<BR> rc\_R49216\_at R49216 2880 EST 3.64 up 0.0004<BR> rc\_R49395\_s\_at R49395 2881 EST 4.38 up 0.00112<BR> rc\_R49476\_at R49476 2883 EST 10.95 up 0.00014<BR> rc\_R52161\_at R52161 2893 EST 5.84 up 0.03253 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_R53109\_f\_at R53109 2899 dimethylarginine dimethylaminohydrolase 2 3.31 up 0.02389<BR> rc\_R53109\_r\_at R53109 2899 dimethylarginine

dimethylaminohydrolase 2 3.22 up 0.00724<BR> rc\_R54614\_s\_at R54614 2902 EST 3.24 up  
 0.00526<BR> rc\_R55470\_at R55470 2904 EST 3.59 up 0.00515<BR> rc\_R56095\_s\_at R56095 2906  
 EST 8.16 up 0.00023<BR> R56678\_at R56678 2908 EST 3.81 up 0.02242<BR> rc\_R56880\_at R56880  
 2909 EST 6.82 up 0.02559<BR> rc\_R58974\_at R58974 2910 EST 4.95 up 0.00498<BR>  
 rc\_R59352\_s\_at R59352 2915 KIAA0296 gene product 4.19 up 0.00393<BR> rc\_r61297\_s\_at R61297  
 2920 eukaryotic translation initiation factor 3, subunit 6 (48kD) 6.42 up 0.00126<BR> R69700\_at  
 R69700 2943 EST 6.71 up 0.0021<BR> rc\_R70005\_at R70005 2944 EST 4.61 up 0.00037<BR>  
 rc\_R70801\_s\_at R70801 2950 EST 6.36 up 0.00563<BR> rc\_R71082\_s\_at R71082 2951 programmed  
 cell death 5 3.6 up 0.01338<BR> rc\_R71395\_at R71395 2952 EST 10.42 up 0.00422<BR>  
 rc\_R73565\_at R73565 2959 EST 3.29 up 0.03489<BR> O-linked N-acetylglucosamine (GlcNAc)  
 transferase (UDP-N-<BR> acetylglucosamine:polypeptide-N-acetylglucosaminyl<BR> rc\_R76782\_s\_at  
 R76782 2963 transferase) 5.83 up 0.01126<BR> rc\_R77631\_at R77631 2967 EST 3.43 up  
 0.00006<BR> rc\_R79580\_at R79580 2970 EST 6.25 up 0.00593<BR> rc\_R87989\_at R87989 2979  
 centrosome associated protein 3.64 up 0.00008<BR> rc\_R91819\_at R91819 2984 EST 8.95 up  
 0.00009<BR> rc\_R92994\_s\_at R92994 2990 matrix metalloproteinase 12 (macrophage elastase) 11.05  
 up 0.00248<BR> rc\_R95966\_i\_at R95966 2997 EST 11.22 up 0.00682<BR> rc\_R96924\_s\_at R96924  
 3001 EST 6.18 up 0.03417<BR> rc\_R97759\_at R97759 3006 serum/glucocorticoid regulated kinase  
 5.99 up 0.00221<BR> S54005\_s\_at S54005 3020 thymosin, beta 10 7.03 up 0.00334<BR> S56151\_s\_at  
 S56151 3021 milk fat globule-EGF factor 8 protein 4.59 up 0.0091<BR> S69272\_s\_at S69272 3028  
 protease inhibitor 6 (placental thrombin inhibitor) 5.15 up 0.00003 Table 6A. Genes up regulated in  
 metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name  
 Fold Change Direction Pvalue<BR> S73885\_s\_at S73885 3032 transcription factor AP-4 (activating  
 enhancer-binding protein 4) 4.18 up 0.00005<BR> S78187\_at S78187 3036 cell division cycle 25B 8.07  
 up 0.00009<BR> s81914\_at S81914 3038 immediate early response 3 5.46 up 0.01798<BR>  
 rc\_T03313\_at T03313 3042 dyskeratosis congenita 1, dyskerin 9.63 up 0.00001<BR> rc\_T03438\_s\_at  
 T03438 3043 EST 8.18 up 0.00032<BR> rc\_T03580\_f\_at T03580 3046 pyruvate kinase, muscle 24.91  
 up 0.0001<BR> rc\_T12599\_f\_at T12599 3056 ribosomal protein L21 3.54 up 0.01437<BR>  
 rc\_T15442\_f\_at T15442 3057 calpain, large polypeptide L1 5.01 up 0.00255<BR> rc\_T15473\_at  
 T15473 3058 muscle specific gene 5.81 up 0.02404<BR> rc\_T15477\_at T15477 3059 EST 3.61 up  
 0.00005<BR> rc\_T15903\_s\_at T15903 3063 EST 3.23 up 0.01377<BR> rc\_T16308\_f\_at T16308 3069  
 EST 5.29 up 0.00119<BR> rc\_T16983\_s\_at T16983 3074 cleavage and polyadenylation specific factor  
 4, 30kD subunit 5.23 up 0.00075<BR> rc\_T23465\_at T23465 3081 EST 4.4 up 0.017<BR>  
 rc\_T23490\_i\_at T23490 3082 EST 11.86 up 0.03242<BR> rc\_T23516\_f\_at T23516 3083 3-  
 phosphoglycerate dehydrogenase 5.38 up 0.00001<BR> rc\_T24068\_s\_at T24068 3088 EST 15.26 up  
 0.00046<BR> rc\_T25725\_at T25725 3091 EST 3.26 up 0.00099<BR> rc\_T26366\_f\_at T26366 3093  
 EST 30.43 up 0.00153<BR> rc\_T26471\_at T26471 3094 EST 4.62 up 0.01091<BR> protein  
 phosphatase 2 (formerly 2A), regulatory subunit A (PR<BR> rc\_T26513\_i\_at T26513 3095 65), alpha  
 isoform 5.07 up 0.0016<BR> rc\_T26574\_s\_at T26574 3096 catenin (cadherin-associated protein), delta  
 1 3.17 up 0.00828<BR> rc\_T30193\_s\_at T30193 3098 protease, serine, 8 (prostasin) 8.39 up  
 0.0043<BR> rc\_T32072\_s\_at T32072 3102 EST 5.95 up 0.00029<BR> rc\_T32108\_at T32108 3103  
 EST 6.96 up 0.00723<BR> rc\_T33489\_s\_at T33489 3105 EST 8.04 up 0.00469<BR> rc\_T33508\_s\_at  
 T33508 3106 phosphatidylinositol-4-phosphate 5-kinase, type II, beta 3.31 up 0.00416 Table 6A. Genes  
 up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known  
 Gene Name Fold Change Direction Pvalue<BR> T35341\_s\_at T35341 3112 EST 4.73 up 0.00057<BR>  
 T35725\_s\_at T35725 3113 EST 3.4 up 0.00149<BR> rc\_T40849\_s\_at T40849 3116 maternal G10  
 transcript 4.11 up 0.00449<BR> rc\_T47032\_s\_at T47032 3124 partner of RAC1 (arfaptin 2) 3.27 up  
 0.00503<BR> rc\_T47325\_s\_at T47325 3125 EST 5.63 up 0.01015<BR> rc\_T47601\_at T47601 3126  
 EST 4.05 up 0.00878<BR> ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-<BR>  
 rc\_T47969\_s\_at T47969 3128 Vogt disease) 3.03 up 0.03452<BR> eukaryotic translation initiation  
 factor 3, subunit 3 (gamma,<BR> T48195\_s\_at T48195 3131 40kD) 3.75 up 0.00012<BR>  
 rc\_T48293\_f\_at T48293 3133 EST 3.55 up 0.01355<BR> rc\_T53404\_at T53404 3143 EST 10.68 up



0.00582<BR> rc\_T55004\_s\_at T55004 3146 EST 4.83 up 0.00156<BR> rc\_T55196\_at T55196 3147 EST 4.04 up 0.00012<BR> rc\_T58153\_s\_at T58153 3154 heat shock 105kD 3.08 up 0.01317<BR> rc\_T58607\_at T58607 3155 EST 3.52 up 0.4102<BR> rc\_T59161\_s\_at T59161 3159 thymosin, beta 10 3.41 up 0.01885<BR> rc\_T59668\_s\_at T59668 3160 lysyl oxidase 3.28 up 0.00588<BR> rc\_T66935\_at T66935 3179 EST 3.97 up 0.00188<BR> rc\_T7733\_s\_at T77733 3219 tubulin, gamma 1 4.42 up 0.00049<BR> rc\_T78922\_s\_at T78922 3222 stem cell growth factor; lymphocyte secreted C-type lectin 3.42 up 0.02419<BR> rc\_T91116\_at T91116 3252 EST 4.01 up 0.02721<BR> rc\_T92935\_at T92935 3255 EST 3.48 up 0.03578<BR> rc\_T95057\_f\_at T95057 3259 EST 10.39 up 0.00003<BR> rc\_T98284\_at T98284 3268 EST 4.47 up 0.00054<BR> U01062\_at U01062 3273 inositol 1,4,5-triphosphate receptor, type 3 7.41 up 0<BR> U01147\_at U01147 3275 active BCR-related gene 3.22 up 0.00103<BR> non-Pou domain-containing octamer (ATGCAAAT) binding<BR> U02493\_at U02493 3279 protein 3.04 up 0.0019 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> U03891\_at U03891 3283 phorbolin (similar to apolipoprotein B mRNA editing protein) 3 up 0.00065<BR> U04313\_at U04313 3284 protease inhibitor 5 (maspin) 4.54 up 0.02986<BR> U05875\_at U05875 3286 interferon gamma receptor 2 (interferon gamma transducer 1) 3.09 up 0.00549<BR> U07969\_s\_at U07969 3289 cadherin 17, LI cadherin (liver-intestine) 10.78 up 0.02002<BR> U09117\_at U09117 3294 phospholipase C, delta 1 7.96 up 0.00001<BR> U09564\_at U09564 3295 SFRS protein kinase 1 3.79 up 0.00765<BR> U09770\_at U09770 3296 cysteine-rich protein 1 (intestinal) 13.03 up 0.0072<BR> U11861\_at U11861 3298 maternal G10 transcript 3.8 up 0.00001<BR> U12404\_at U12404 3299 ribosomal protein L10a 4.18 up 0.00004<BR> U12465\_at U12465 3300 ribosomal protein L35 4.69 up 0.00001<BR> U14968\_at U14968 3303 ribosomal protein L27a 4.01 up 0.00003<BR> U14969\_at U14969 3304 ribosomal protein L28 4.63 up 0.00004<BR> U14970\_at U14970 3305 ribosomal protein S5 3.45 up 0.00915<BR> U14971\_at U14971 3306 ribosomal protein S9 3.93 up 0.00026<BR> U14972\_at U14972 3307 ribosomal protein S10 5.24 up 0.00077<BR> U14973\_at U14973 3308 ribosomal protein S29 3.1 up 0.00028<BR> U15008\_at U15008 3309 small nuclear ribonucleoprotein D2 polypeptide (16.5kd) 4.9 up 0.00396<BR> U17077\_at U17077 3314 BENE protein 4.98 up 0.00366<BR> laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600<BR> U17760\_ma1\_at U17760 3315 (125kD)) 3.54 up 0.01853<BR> U20499\_at U20499 3321 sulfotransferase family 1A, phenol-preferring, member 3 5.5 up 0.00299<BR> secreted phosphoprotein 1 (osteopontin, bone sialoprotein I,<BR> U20758\_ma1\_at U20758 3323 early T-lymphocyte activation 1) 6.12 up 0.03448<BR> epithelial protein up-regulated in carcinoma, membrane<BR> U21049\_at U21049 3325 associated protein 17 7.53 up 0.01667<BR> U22376\_cds2\_s\_at U22376 3328 v-myb avian myeloblastosis viral oncogene homolog 3.34 up 0.03416<BR> U25789\_at U25789 3334 ribosomal protein L21 4.37 up 0.00045 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> U26726\_at U26726 3336 hydroxysteroid (11-beta) dehydrogenase 2 3.45 up 0.02342<BR> fucosyltransferase 3 (galactoside 3(4)-L-flucosyltransferase,<BR> U27328\_s\_at U27328 3338 Lewis blood group included) 3.05 up 0.03224<BR> U31556\_at U31556 3346 E2F transcription factor 5, p130-binding 4.14 up 0.01157<BR> U33286\_at U33286 3349 chromosome segregation 1 (yeast homolog)-like 3.39 up 0.00939<BR> solute carrier family 6 (neurotransmitter transporter, creatine),<BR> U36341\_ma1\_at U36341 3351 member 8 3.05 up 0.02622<BR> U37689\_at U37689 3356 polymerase (RNA) II (DNA directed) polypeptide H 3.65 up 0.00044<BR> potassium voltage-gated channel, KQT-like subfamily, member<BR> U40990\_at U40990 3359 1 3.18 up 0.00093<BR> U42408\_at U42408 3361 laminin 1 6.8 up 0.00305<BR> U43901\_ma1\_s\_at U43901 3362 laminin receptor 1 (67kD, ribosomal protein SA) 3.11 up 0.03145<BR> U46692\_ma1\_at U46692 3367 cystatin B (stein B) 5.54 up 0.00016<BR> U47025\_s\_at U47025 3368 phosphorylase, glycogen; brain 8.52 up 0.00134<BR> U48705\_ma1-s\_at U48705 3370 discoidin domain receptor family, member 1 5.94 up 0.01323<BR> U51095\_at U51095 3382 caudal type homeo box transcription factor 1 4.76 up 0.02664<BR> U51478\_at U51478 3385 ATPase, Na<sup>+</sup>/K<sup>+</sup> transporting, beta 3 polypeptide 5.75 up 0.00007<BR> solute carrier family 1 (neutral amino acid transporter), member<BR> U53347\_at



U53347 3389 5 3.81 up 0.00273<BR> U53830\_at U53830 3391 interferon regulatory factor 7 3.94 up  
 0.03147<BR> U58682\_at U58682 3396 ribosomal protein S28 6.09 up 0.00001<BR> U62392\_at  
 U62392 3403 zinc finger protein 193 3.18 up 0.00269<BR> U62962\_at U62962 3404 eukaryotic  
 translation initiation factor 3, subunit 6 (48kD) 4.05 up 0.0047<BR> U67171\_at U67171 3409  
 selenoprotein W, 1 3.08 up 0.0047<BR> U73379\_at U73379 3418 ubiquitin carrier protein E2-C 8.32  
 up 0.00101<BR> U73843\_at U73843 3421 E74-like factor 3 (ets domain transcription factor) 5.75 up  
 0.00017<BR> U75285\_ma1\_at U75285 3422 apoptosis inhibitor 4 (survivin) 4.46 up 0.02212<BR>  
 U76366\_s\_at U76366 3424 Treacher Collins-Franceschetti syndrome 1 3.44 up 0.00021<BR>  
 U78027\_ma3\_at U78027 3429 EST 4.15 up 0.00295<BR> U78095\_at U78095 3430 serine protease  
 inhibitor, Kunitz type, 2 18.85 up 0 Table 6A. Genes up regulated in metastatic tissue versus normal  
 sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction  
 Pvalue<BR> U78525\_at U78525 3432 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)  
 4.68 up 0.00132<BR> U78556\_at U78556 3433 cisplatin resistance associated 5.77 up 0.00241<BR>  
 U79266\_at U79266 3434 protein predicted by clone 23627 3.49 up 0.00004<BR> U79725\_at U79725  
 3438 glycoprotein A33 (transmembrane) 8.57 up 0.00299<BR> U83246\_at U83246 3443 copine I 3.57  
 up 0.01672<BR> U84720\_at U84720 3446 RAE1 (RNA export 1, S:pombe) homolog 3.37 up  
 0.03586<BR> U85773\_at U85773 3449 phosphomannomutase 2 3.94 up 0.00288<BR> U86409\_at  
 U86409 3450 EST 3.38 up 0.00003<BR> U89606\_at U89606 3452 pyridoxal (pyridoxine, vitamin B6)  
 kinase 3.57 up 0.00322<BR> U90549\_at U90549 3456 high-mobility group (nonhistone chromosomal)  
 protein 17-like 3 3.2 up 0.0401<BR> U90913\_at U90913 3459 Tax interaction protein 1 4.35 up  
 0.00159<BR> U93205\_at U93205 3461 chloride intracellular channel 1 6.14 up 0.00058<BR>  
 U93686\_at U93686 3463 polymerase (RNA) III (DNA directed) (32kD) 3.5 up 0.01235<BR>  
 rc\_W02041\_at W02041 3466 EST 4.83 up 0.00158<BR> rc\_W20391\_s\_at W20391 3479 kinesin-like 2  
 3.98 up 0.01788<BR> W28362\_at W28362 3488 KIAA0974 protein 3.98 up 0.00626<BR>  
 rc\_W31382\_at W31382 3495 EST 4 up 0.00058<BR> rc\_W37680\_at W37680 3503 EST 3.55 up  
 0.01036<BR> rc\_W37937\_at W37937 EST 3.07 up 0.00776<BR> myeloid/lymphoid or mixed-lineage  
 leukemia (trithorax<BR> rc\_W38044\_s\_at W38044 (Drosophila) homolog); translocated to, 7 7.28 up  
 0.03105<BR> W39183\_s\_at W39183 3508 KIAA0601 protein 3.66 up 0.00018<BR> rc\_W42627\_f\_at  
 W42627 3511 EST 3.56 up 0.00198<BR> rc\_W42957\_at W42957 3516 calmodulin 2 (phosphorylase  
 kinase, delta) 15.22 up 0.00007<BR> rc\_W44557\_at W44557 3518 chromosome 1 open reading frame 2  
 4.32 up 0.00128<BR> rc\_W44733\_at W44733 3519 EST 3.02 up 0.00097<BR> rc\_W45487\_s\_at  
 W45487 3524 dynamin 2 4.2 up 0.00325<BR> rc\_W49574\_at W49574 3538 EST 5.97 up  
 0.00045<BR> rc\_W49661\_s\_at W49661 3539 FK506-binding protein 9 (63 kD) 3.01 up 0.02259 Table  
 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq  
 ID Known Gene Name Fold Change Direction Pvalue<BR> W52858\_at W52858 3545  
 DKFZP564F0522 protein 4.38 up 0.00088<BR> rc\_W60486\_at W60486 3558 EST 4.29 up  
 0.00964<BR> rc\_W67251\_s\_at W67251 3570 EST 6.13 up 0.01463<BR> rc\_W70336\_at W70336 3579  
 EST 3.65 up 0.01776<BR> rc\_W72276\_at W72276 3583 EST 27.39 up 0.00183<BR> protein tyrosine  
 phosphatase, receptor type, f polypeptide<BR> rc\_W72861\_at W72861 3586 (PTPRF), interacting  
 protein (liprin), alpha 3 3.0 up 0.00055<BR> rc\_W73189\_at W73189 3589 EphB2 3.69 up  
 0.02909<BR> rc\_W73914\_at W73914 3595 EST 3.5 up 0.04782<BR> rc\_W74233\_s\_at W74233 3597  
 related RAS viral (r-ras) oncogene homolog 6.02 up 0.01815<BR> W76097\_at W76097 3599 EST 3.83  
 up 0.00001<BR> rc\_W78057\_at W78057 3600 EST 9.06 up 0.0034<BR> rc\_W80730\_at W80730 3607  
 EST 6.59 up 0.00425<BR> rc\_W80763\_at W80763 3608 EST 3.83 up 0.01319<BR> rc\_W81375\_at  
 W81375 3613 EST 3.58 up 0.00322<BR> rc\_W81540\_at W81540 3614 serine/threonine kinase 24  
 (Ste20, yeast homolog) 6.72 up 0.00164<BR> rc\_W90146\_f\_at W90146 3644 EST 6.23 up  
 0.01558<BR> rc\_W92207\_at W92207 3651 EST 6.77 up 0.00002<BR> rc\_W92449\_at W92449 3652  
 EST 31.67 up 0.00011<BR> rc\_W92608\_s\_at W92608 3653 BAI1-associated protein 3 5.12 up  
 0.00075<BR> rc\_W93726\_s\_at W93726 3656 protease inhibitor 5 (maspin) 16.48 up 0.00014<BR>  
 rc\_W93943\_at W93943 3657 EST 4.3 up 0.00296<BR> W95348\_at W95348 3663 HSPC113 protein  
 10.89 up 0.01065<BR> rc\_W95477\_at W95477 3664 EST 26.51 up 0.00161<BR> X03342\_at X03342

3675 ribosomal protein L32 4.09 up 0.00008<BR> AFFX-CreX-5\_at x03453 3677 EST 3.03 up 0.0025<BR> X04347\_s\_at X04347 3680 heterogeneous nuclear ribonucleoprotein A1 7.26 up 0.00018<BR> X05610\_at X05610 3685 collagen, type IV, alpha 2 3.58 up 0.01351<BR> X06617\_at X06617 3687 ribosomal protein S11 4.32 up 0.0002<BR> X07820\_at X07820 3695 matrix metalloproteinase 10 (stromelysin 2) 3.49 up 0.00689 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> X12447\_at X12447 3696 aldolase A, fructose-bisphosphate 10.52 up 0.00038<BR> X13956\_at X13956 3701 EST 3.2 up 0.00321<BR> X14850\_at X14850 3706 H2A histone family, member X 4.11 up 0.0001<BR> X15940\_at X15940 3709 ribosomal protein L31 4.45 up 0.0004<BR> X17093\_at X17093 3716b EST 4.82 up 0.00176<BR> X17206\_at X17206 3718 ribosomal protein S2 5.14 up 0<BR> X17567\_s\_at X17567 3719 small nuclear ribonucleoprotein polypeptides B and B1 3.6 up 0.00586<BR> X51466\_at X51466 3720 eukaryotic translation elongation factor 2 3.25 up 0.00019<BR> X51521\_at X51521 3721 villin 2 (ezrin) 3.89 up 0.0001<BR> X52851\_mal\_at X52851 3725 EST 3.38 up 0.0001<BR> X52966\_at X52966 3726 ribosomal protein L35a 3.93 up 0.00217<BR> X53331\_at X53331 3727 matrix Gla protein 3.66 up 0.04038<BR> X54667\_s\_at X54667 3731 cystatin S, cystatin SN 8.53 up 0.00059<BR> X55715\_at X55715 3735 ribosomal protein S3 3.72 up 0.00755<BR> X55954\_at X55954 3736 ribosomal protein L23 3.81 up 0.00025<BR> X56494\_at X56494 3738 pyruvate kinase, muscle 22.97 up 0.00001<BR> X56932\_at X56932 3740 ribosomal protein L13a 3.26 up 0<BR> X56997\_mal\_at X56997 3741 ubiquitin A-52 residue ribosomal protein fusion product 1 3.18 up 0.0006<BR> X57348\_s\_at X57348 3744 stratifin 12.53 up 0.0013<BR> X62535\_at X62535 3756 diacylglycerol kinase, alpha (80kD) 4.72 up 0.00315<BR> X62691\_at X62691 3757 ribosomal protein S15a 4.09 up 0.00004<BR> X63627\_at X63527 3761 ribosomal protein L19 3.17 up 0.02488<BR> X63629\_at X63629 3762 cadherin 3, P-cadherin (placental) 3.02 up 0.01654<BR> X64364\_at X64364 3764 basigin 6.45 up 0.00041<BR> X64707\_at X64707 3765 ribosomal protein L13 4.28 up 0.00257<BR> X65614\_at X65614 3767 S100 Calcium-binding protein P 12.2 up 0.00056<BR> X66364\_at X66364 3770 cyclin-dependent kinase 5 3.55 up 0.02824<BR> proteasome (prosome, macropain) subunit, beta type, 9 (large<BR> X66401\_cds1\_at X66401 3771 multifunctional protease 2) 3.68 up 0.01385<BR> X66899\_at X66899 3772 Ewing sarcoma breakpoint region 1 4.72 up 0.00011 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> X67247\_mal\_at X67247 3774 mitogenactivated protein kinase kinase kinase kinase 3 3.48 up 0.00012<BR> X67325\_25 X67325 3775 interferon, alpha-inducible protein 27 9.67 up 0.03245<BR> X68314\_at X68314 3778 glutathione peroxidase 2 (gastrointestinal) 14.4 up 0.00222<BR> X68688\_mal\_s\_at X68688 3780 zinc finger protein 33a (KOX 31) 4.7 up 0.00062<BR> X68668\_mal\_s\_at X68688 3780 zinc finger protein 33a (KOX 31) 3.62 up 0.00319<BR> X69150\_at X69150 3782 ribosomal protein S18 4.5 up 0.00003<BR> X69391\_at X69391 3783 ribosomal protein L6 3.18 up 0.00004<BR> CD47 antigen (Rh-related antigen, integrin-associated signal<BR> X69398\_at X69398 3784 transducer) 3.68 up 0.02332<BR> X69654\_at X69654 3785 ribosomal protein S26 3.11 up 0.02683<BR> ATP synthase, H<sup>+</sup> transporting, mitochondrial F0 complex,<BR> X69908\_mal\_at X69908 3786 subunit c (subunit 9), isoform 2 3.73 up 0.00685<BR> macrophage stimulating 1 receptor (c-met-related tyrosine<BR> X70040\_at X70040 3788 kinase) 4 up 0.00402<BR> X74929\_s\_at X74929 3792 keratin 8 4.73 up 0.00018<BR> X76180\_at X76180 3795 sodium channel, nonvoltage-gated 1 alpha 11.68 up 0<BR> X77588\_s\_at X77588 3799 N-acetyltransferase, homolog of S. cerevisiae ARD1 3.91 up 0.0221<BR> X78687\_at X78687 3800 sialidase 1 (lysosomal sialidase) 3.18 up 0.031<BR> X79234\_at X79234 3803 ribosomal protein L11 3.59 up 0.00051<BR> X79882\_at X79882 3805 lung resistance-related protein 6.71 up 0.0362<BR> X8198\_at X80198 3807 steroidogenic acute regulatory protein related 3.03 up 0.00044<BR> X80822\_at X80822 3808 ribosomal protein L18a 4.13 up 0.0006<BR> X80822\_f\_at X80822 3808 ribosomal protein L18a 3.08 up 0.02481<BR> X80909\_at X80909 3809 nascent-polypeptide-associated complex alpha polypeptide 3.84 up 0.00399<BR> X833228\_at X833228 3810 cadherin 17, LI cadherin (liver-Intestine) 10.58 up 0.02147<BR> X89960\_at X89960 3818 EST 9.87 up 0<BR> high-mobility group (nonhistone

chromosomal) protein isoform I0-<BR> X92518\_s\_at X92518 3825 C 3.12 up 0.00638<BR> X93036\_at X93036 3830 FXFD domain-containing ion transport regulator 3 42.36 up 0.00167 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction pvalue<BR> X95404\_at X95404 3834 cofilin 1 (non-muscle) 3.18 up 0.00104<BR> X98482\_r\_at X98482 3841 EST 5.03 up 0.00002<BR> X99133\_at X99133 3842 lipocalin 2 (oncogene 24p3) 6.27 up 0.0453<BR> Y00503\_at Y00503 3849 keratin 19 14.19 up 0.00217<BR> Y00705\_at Y00705 3850 serine protease inhibitor, Kazal type 1 9.83 up 0.03697<BR> Y10807\_s\_at Y10807 3860 HMT1 (hnRNP methyltransferase, *S. cerevisiae*)-like 2 4.28 up 0.00124<BR> Z23090\_at Z23090 3868 heat shock 27kD protein 1 7.67 up 0.00008<BR> Z24727\_at Z24727 3871 tropomyosin 1 (alpha) 4.47 up 0.00121<BR> nuclear factor of kappa light polypeptide gene enhancer in B-<BR> Z25749\_rna1\_at Z25749 3872 cells inhibitor-like 2 4.41 up 0.00031<BR> Z26876\_at Z26876 3874 ribosomal protein L38 4.43 up 0.00022<BR> Z28407\_at Z28407 3876 ribosomal protein L8 6.3 up 0.00004<BR> Z30643\_at Z30643 3879 chloride channel Ka 3.86 up 0.00204<BR> rc\_Z38150\_s\_at Z38150 3883 EST 3.06 up 0.00049<BR> rc\_Z38266\_at Z38266 3886 EST 6.58 up 0.01909<BR> rc\_Z38729\_at Z38729 3894 EST 3.13 up 0.04514<BR> rc\_Z38909\_at Z38909 3897 EST 3.55 up 0.03195<BR> rc\_Z39079\_at Z39079 3900 KIAA1058 protein 4.08 up 0.01781<BR> rc\_Z39191\_at Z39191 3901 EST 8.84 up 0.00011<BR> rc\_Z39200\_at Z39200 3902 EST 3.29 up 0.00586<BR> rc\_Z39429\_at Z39429 3906 EST 7.84 up 0.00045<BR> rc\_Z39930\_f\_at Z39930 3914 EST 3.07 up 0.00002<BR> rc\_Z40583\_f\_at Z40583 3922 EST 4.24 up 0.02375<BR> rc\_Z40898\_at Z40898 3925 EST 3.71 up 0.01168<BR> rc\_Z40945\_at Z40945 3927 trinucleotide repeat containing 15 7.82 up 0.00007<BR> rc\_Z41103\_at Z41103 3929 trinucleotide repeat containing 15 3.83 up 0.00444<BR> rc\_Z41740\_s\_at Z41740 3935 EST 6.76 up 0.00049<BR> rc\_Z41798\_s\_at Z41798 3937 EST 6.7 up 0.00073<BR> Z68228\_s\_at Z68228 3947 junction plakoglobin 3.3 up 0.0237<BR> Z74615\_at Z74615 3949 collagen, type I, alpha 1 10.47 up 0.00064<BR> Z74616\_s\_at Z74616 3950 collagen, type I, alpha 2 4.83 up 0.02364 Table 6B. Down regulated in metastatic cancer sversus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA001603\_at AA001603 3 EST 4.31 down 0.00883<BR> rc\_AA001604\_at AA001604 4 EST 3.33 down 0.0215<BR> AA004231\_at AA004231 7 EST 3.16 down 0.03067<BR> rc\_AA004521\_at AA004521 8 prostate cancer overexpressed gene 1 8.03 down 0.00027<BR> rc\_AA004905\_at AA004905 11 KIAA0937 protein 4.63 down 0.00082<BR> rc\_AA005202\_at AA005202 12 retinol-binding protein 4, interstitial 3.18 down 0.00106<BR> rc\_AA005358\_at AA005358 14 EST 5.2 down 0.00138<BR> rc\_AA007629\_at AA007629 19 EST 8.01 down 0.00001<BR> rc\_AA009719\_at AA009719 20 peroxisomal membrane protein 2 (22kD) 47.12 down 0.00008<BR> rc\_AA010205\_at AA010205 23 EST 7.41 down 0<BR> rc\_AA010360\_at AA010360 24 EST 6.55 down 0.00027<BR> rc\_AA010530\_at AA010530 25 EST 3.74 down 0.0481<BR> rc\_AA010619\_at AA010619 27 EST 8.55 down 0.00057<BR> AA010750\_at AA010750 28 calmodulin 1 (phosphorylase kinase, delta) 10.22 down 0.00959<BR> rc\_AA015768\_at AA015768 34 EST 15.3 down 0.00008<BR> rc\_AA017146\_at AA017146 36 EST 10.1 down 0.00052<BR> rc\_AA017192\_at AA017192 37 EST 3.43 down 0.04865<BR> rc\_AA018867\_at AA018867 39 EST 42.87 down 0.00002<BR> rc\_AA021623\_s\_at AA021623 43 insulin induced gene 1 11.71 down 0.00094<BR> rc\_AA025930\_at AA025930 52 EST 3.59 down 0.00372<BR> rc\_AA031543\_s\_at AA031543 68 translocation protein 1 5.92 down 0.00405<BR> AA031548\_at AA031548 68 cell division cycle 42 (GTP-binding protein, 25kD) 3.65 down 0.03029<BR> rc\_AA032005\_at AA032005 71 EST 5.3 down 0.01202<BR> AA032048\_at AA032048 72 EST 5.45 down 0.00383<BR> rc\_AA032250\_at AA032250 73 EST 3.56 down 0.0009<BR> rc\_AA034030\_at AA034030 75 methylmalonyl Coenzyme A mutase 14.32 down 0.00004<BR> rc\_AA035245\_s\_at AA035245 79 aldehyde oxidase 1 69.82 down 0.00117<BR> rc\_AA035457\_at AA035457 80 EST 10.06 down 0.00085<BR> rc\_AA035638\_at AA035638 82 EST 9.91 down 0.00541<BR> rc\_AA036662\_s\_at AA036662 83 EST 4.16 down 0.00235<BR> rc\_AA037357\_f\_at AA037357 85 EST 3.53 down 0.02129 Table 6B. Down regulated in metastatic cancer sversus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA039335\_s\_at

AA039335 89 coagulation factor XII (Hageman factor) 32 down 0.0029<BR> rc\_AA039616\_at  
AA039616 90 eST 9.36 down 0.00009<BR> AA039806\_at AA039806 91 msh (Drosophila) homeo box  
homolog 1 3.53 down 0.00114<BR> rc\_AA040087\_at AA040087 92 EST 4.13 down 0.00123<BR>  
rc\_AA040270\_at AA040270 93 EST 3.03 down 0.01367<BR> rc\_AA040291\_at AA040291 94  
KIAA0669 gene product 3.55 down 0.00308<BR> rc\_AA043501\_at AA043501 98 v-maf  
musculoaponeurotic fibrosarcoma (avian) 3.81 down 0.01304<BR> AA044622\_at AA044622 103 EST  
3.62 down 0.03789<BR> AA044755\_s\_at AA044755 104 EST 6.7 down 0.01228<BR> AA044842\_at  
AA044842 105 Autosomal Highly Conserved protein 5.231 down 0.0009<BR> AA045870\_at  
AA045870 108 EST 5.93 down 0.00017<BR> rc\_AA046457\_at AA046457 111 EST 3.2 down  
0.00513<BR> AA046674\_at AA046674 112 EST 5.17 down 0.02561<BR> rc\_AA046747\_at  
AA046747 114 EST 4.82 down 0.00022<BR> AA046840\_at AA046840 115 CCAAT/enhancer binding  
protein (C/EBP). delta 3.79 down 0.03319<BR> AA047151\_at AA047151 116 EST 7.13 down  
0.00007<BR> rc\_AA047187\_at AA047187 117 EST 3.04 down 0.04306<BR> rc\_AA047290\_at  
AA047290 118 EST 3.39 down 0.00024<BR> rc\_AA052980\_at AA052980 122 EST 4.52 down  
0.023<BR> rc\_AA055992\_at AA055992 136 calumenin 3.51 down 0.0064<BR> AA056170\_at  
AA056170 137 EST 3.82 down 0.0083<BR> rc\_AA056247\_at AA056247 138 EST 3.48 down  
0.03277<BR> rc\_AA056482\_at AA056482 141 EST 4.82 down 0.00199<BR> rc\_AA057678\_at  
AA057678 143 EST 6.88 down 0.00078<BR> AA059489\_at AA059489 145 RGC32 protein 3.74 down  
0.00734<BR> rc\_AA062744\_at AA062744 147 EST 3.31 down 0.01909<BR> rc\_AA065173\_at  
AA065173 148 EST 4.08 down 0.00377<BR> rc\_AA069456\_at AA069456 149 KIAA0438 gene  
product 3.47 down 0.02718<BR> rc\_AA069768\_s\_at AA069768 151 hevin 4.62 down 0.00202<BR>  
AA070090\_at AA070090 152 EST 3.24 down 0.00804<BR> rc\_AA070091\_at AA070091 153 EST 5  
down 0 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID  
Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA074885\_at AA074885  
161 macrophage receptor with collagenous structure 11.05 down 0.00786<BR> rc\_AA074891\_at  
AA074891 162 EST 3.12 down 0.01897<BR> rc\_AA076238\_at AA076238 168 EST 3.23 down  
0.00395<BR> rc\_AA076249\_at AA076249 169 TST 3.78 down 0.00029<BR> rc\_AA076326\_at  
AA076326 170 SEC14 (S. Cerevisiae)-like 2 10.88 down 0.00616<BR> solute carrier family 25  
(mitochondrial carrier;<BR> rc\_AA079758\_f\_at AA079758 174 citrate transporter), member 1 7.83  
down 0.00359<BR> rc\_AA083812\_at AA083812 175 DKFZP566F 123 protein 9.11 down  
0.00167<BR> rc\_AA084408\_at AA084408 179 EST 4.05 down 0.00864<BR> rc\_AA084668\_at  
AA084668 180 ubiquitin-like 3 3.19 down 0.0419<BR> rc\_AA085987\_s\_at AA085987 183 UDP  
glycosyltransferase 1 40.87 down 0.00004<BR> rc\_AA086201\_at AA086201 185 EST 5.8 down  
0.00012<BR> rc\_AA088698\_at AA088698 188 EST 3.23 down 0.02543<BR> AA090257\_at  
AA090257 190 superoxide dismutase 2, mitochondrial 11.72 down 0.02072<BR> AA090434\_at  
AA090434 191 diaphanous (Drosophila, homolog) 1 4.61 down 0.01704<BR> AA090439\_at  
AA090439 192 ribosomal protein S6 5.58 down 0.00501<BR> AA092596\_at AA092596 197 bone  
morphogenetic protein 6 3.46 down 0.02532<BR> AA092716\_at AA092716 198 HLA-B associated  
transcript-3 13.97 down 0.0009<BR> AA093923\_at AA093923 200 EST 3.82 down 0.03924<BR>  
AA094507\_s\_at AA094507 201 EST 3.52 down 0.04783<BR> AA094999\_at AA094999 204 zinc  
finger protein 216 5.12 down 0.0257<BR> rc\_AA099225\_at AA099225 206 EST 7.33 down  
0.00062<BR> AA099391\_s\_at AA099391 207 myosin, light polypeptide kinase 9.07 down  
0.00003<BR> rc\_AA099589\_s\_at AA099589 210 GDP dissociation inhibitor 2 3.7 down 0.04069<BR>  
rc\_AA101055\_s\_at AA101055 213 leptin receptor 3.14 down 0.0071<BR> rc\_AA101235\_at  
AA101235 214 EST 8.46 down 0.00822<BR> rc\_AA101632\_at AA101632 217 EST 4.19 down  
0.00023<BR> rc\_AA112101\_f\_at AA112101 222 EST 8.5 down 0.00004<BR> rc\_AA112209\_s\_at  
AA112209 223 acyl-Coenzyme A dehydrogenase, long chain 3.37 down 0.00084<BR> UDP-N-  
acetylglucosamine pyrophosphorylase 1;<BR> AA114949\_at AA114949 228 Sperm associated antigen  
2 5.12 down 0.01028 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR>  
<P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA121140\_at  
AA121140 235 EST 3.33 down 0.00058<BR> rc\_aa122345\_f\_at AA122345 238 glutamate

dehydrogenase 1 16.53 down 0.00004<BR> rc\_AA125831\_r\_at AA125831 241 myosin, light  
 polypeptide kinase 8.18 down 0.00039<BR> rc\_AA125856\_at AA125856 242 EST 3.17 down  
 0.01545<BR> rc\_AA125861\_at AA125861 243 EST 3.69 down 0.01547<BR> rc\_AA126059\_at  
 AA126059 246 EST 3.08 down 0.00706<BR> rc\_AA126722\_s\_at AA126722 251 O-6-methylguanine-  
 DNA methyltransferase 8.26 down 0.002<BR> rc\_AA127444\_at AA127444 252 EST 3.56 down  
 0.0291<BR> rc\_AA127514\_at AA127514 253 EST 3.4 down 0.00045<BR> rc\_AA133215\_at  
 AA132215 277 calcitonin receptor-like receptor activity modifying 4.55 down 0.02092<BR>  
 rc\_AA133296\_at AA133296 278 EST 4.23 down 0.00041<BR> rc\_AA133439\_at AA133439 279 EST  
 4.07 down 0.00022<BR> rc\_AA134549\_at AA134549 288 EST 3.36 down 0.03438<BR>  
 rc\_AA135558\_s\_at AA135558 293 peptidase D 4.17 down 0.0068<BR> rc\_AA135958\_at AA135958  
 296 EST 4.02 down 0.00012<BR> rc\_AA136079\_at AA136079 297 EST 4.26 down 0.0057<BR>  
 rc\_AA142849\_at AA142849 306 EST 7.59 down 0.00804<BR> AA143019\_at AA143019 309 EST  
 6.75 down 0.00109<BR> rc\_AA147646\_s\_at AA147646 317 DKFZP586A0522 protein 21.82 down  
 0<BR> rc\_AA148480\_s\_at AA148480 318 flavin containing monooxygenase 5 19.64 down 0<BR>  
 rc\_AA148923\_at AA148923 321 decidual protein induced by progesterone 13.2 down 0.00257<BR>  
 rc\_AA149253\_at AA149253 323 EST 5.12 down 0.00863<BR> rc\_AA150776\_at AA150776 330 EST  
 10.45 down 0.00015<BR> rc\_AA150891\_at AA150891 331 EST 4.22 down 0.01692<BR>  
 rc\_AA151210\_at AA151210 333 EST 4.61 down 0.00008<BR> rc\_AA151676\_at AA151676 337  
 peptidyl arginine deiminase, type II 4.01 down 0.00911<BR> rc\_AA156336\_at AA156336 341 nuclear  
 receptor co-repressor 1 3.69 down 0.01276<BR> 4-nitrophenylphosphatase domain and non-  
 rc\_AA156656\_at AA156656 344 neuronal SNAP25-like 1 15.01 down 0.01387<BR> rc\_AA157112\_at  
 AA157112 345 EST 3.94 down 0.02571<BR> AA157520\_at AA157520 347 EST 3.18 down 0.00516  
 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank  
 Seq ID Known Gene Name Fold Change Direction Pvalue<BR> aldo-keto reductase family 7, member  
 A2<BR> rc\_AA157799\_at AA157799 348 (aflatoxin aldehyde reductase) 5.96 down 0<BR>  
 rc\_AA164586\_s\_at AA164586 359 estrogen receptor 1 5.8 down 0.0182<BR> rc\_AA167565\_at  
 AA167565 362 EST 8.08 down 0.00046<BR> rc\_AA171694\_at AA171694 366 ceruloplasmin  
 (ferroxidase) 21.23 down 0.00179<BR> rc\_AA172372\_at AA172372 370 EST 6.48 down  
 0.00344<BR> rc\_AA176233\_at AA176233 376 EST 11.44 down 0.01856<BR> rc\_AA179004\_at  
 AA179004 377 EST 14.34 down 0.00008<BR> rc\_AA179387\_at AA179387 379 DKFZP434N126  
 protein 3.7 down 0.01588<BR> rc\_AA180356\_at AA180356 382 EST 3.16 down 0.00917<BR>  
 rc\_AA182030\_at AA182030 387 EST 8.32 down 0.00018<BR> rc\_AA182568\_at AA182568 388  
 STAT induced STAT inhibitor-2 10.92 down 0.00099<BR> AA188921\_at AA188921 393 similar to  
 Caenorhabditis elegans protein 4.05 down 0.004<BR> rc\_AA190816\_at AA190816 398 EST 4.1 down  
 0.00037<BR> rc\_AA191014\_at AA191014 396 EST 5.07 down 0.01455<BR> protein phosphatase 2  
 (formerly 2A), regulatory<BR> rc\_AA191310\_s\_at AA191310 397 subunit A (PR 65), beta isoform  
 7.28 down 0<BR> rc\_AA191488\_s\_at AA191488 398 solute carrier family 31 (copper transporters),  
 3.19 down 0.00013<BR> rc\_AA191647\_at AA191647 399 ceruloplasmin (ferroxidase) 4.05 down  
 0.00029<BR> rc\_AA193204\_at AA193204 402 Arg/Abl-interacting protein ArgBP2 8.98 down  
 0.00861<BR> rc\_AA193223\_at AA193223 403 EST 4.2 down 0.02416<BR> AA193297\_at AA193297  
 404 EST 4.37 down 0.04676<BR> rc\_AA194075\_f\_at AA194075 406 nuclear receptor coactivator 4  
 4.69 down 0.00862<BR> AA194146\_at AA194146 407 EST 3.53 down 0.000352<BR>  
 rc\_AA194833\_at AA194833 411 claudin 1 11.45 down 0.00034<BR> rc\_AA194997\_s\_at AA194997  
 412 EST 16.12 down 0.00103<BR> rc\_AA195656\_at AA195656 418 KIAA0977 protein 15.29 down  
 0.00817<BR> rc\_AA195657\_at AA195657 419 EST 6.44 down 0.00016<BR> rc\_AA196287\_at  
 AA196287 420 EST 15.07 down 0.00001<BR> intercellular adhesion molecule 1 (CD54), human<BR>  
 rc\_AA197311\_s\_at AA197311 1422 rhinovirus receptor 6.07 down 0.00053 Table 6B. Down regulated in  
 metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name  
 Fold Change Direction Pvalue<BR> FERM, RhoGEF (ARHGEF) and pleckstrin<BR> AA203222\_at  
 AA203222 424 domain protein 1 (chondrocyte-derived) 4.21 down 0.00745<BR> rc\_AA205724\_at  
 AA205724 426 EST 6.73 down 0.00027<BR> rc\_AA207123\_at AA207123 430 immunoglobulin



superfamily, member 3 3.16 down 0.00328<BR> rc\_AA210850\_at AA210850 431 EST 4.97 down 0.00735<BR> rc\_AA211388\_at AA211388 433 EST 4.56 down 0.02703<BR> rc\_AA214542\_at AA214542 438 EST 4.43 down 0.00601<BR> rc\_AA215585\_s\_at AA215585 442 nudix (nucleoside diphosphate linked moiety X)- 3 down 0.03027<BR> AA215919\_at AA215919 443 F-box protein 7 6.62 down 0.00921<BR> rc\_AA218727\_at AA218727 445 EST 3.47 down 0.00125<BR> rc\_AA219039\_at AA219039 446 EST 5.76 down 0.00053<BR> rc\_AA219304\_s\_at AA219304 447 alpha-2-macroglobulin 21.97 down 0.00011<BR> rc\_AA219656\_at AA219653 448 EST 4.08 down 0.00607<BR> rc\_AA223335\_s\_at AA223335 449 propionyl Coenzyme A carboxylase, beta 5.49 down 0.2761<BR> rc\_AA223902\_at AA22392 450 EST 9.91 down 0.00003<BR> rc\_AA227452\_at AA227452 445 EST 4.7 down 0.02345<BR> rc\_AA227480\_s\_at AA22748 456 pim-2 oncogene 3.31 down 0.02413<BR> rc\_AA227901\_at AA227901 459 SEC24 (S. cerevisiae) related gene family, 3.18 down 0.00397<BR> rc\_AA228119\_at AA228119 462 pre-B-ceol colony-enhancing factor 4.77 down 0.00031<BR> rc\_AA232114\_s\_at AA232114 463 epoxide hydrolase 2, cytoplasmic 24.34 down 0.00007<BR> rc\_AA233152\_at AA233152 467 EST 12.95 down 0<BR> rc\_AA233347\_at AA233347 470 zinc finger protein 216 5.9 down 0.0041<BR> rc\_AA233369\_at AA233369 471 histidine ammonia-lyase 9.06 down 0.0008<BR> rc\_AA233763\_at AA233763 472 EST 4.61 down 0.00004<BR> rc\_AA233837\_at AA233837 474 EST 4.79 down 0.0034<BR> rc\_AA234095\_at AA234095 478 EST 8.08 down 0.00394<BR> rc\_AA234527\_s\_at AA234527 483 nuclear receptor subfamily 3, group C, member 1 6.19 down 0.00864<BR> rc\_AA234561\_at AA234561 485 EST 3.88 down 0.02058<BR> AA234634\_f\_at AA234634 486 CCAAT/enhancer binding protein (C/EBP), delta 7.48 down 0.03318<BR> AA234817\_at AA234817 490 EST 6.22 down 0.00099<BR> rc\_AA234831\_at AA234831 491 EST 3.42 down 0.00206 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA234916\_at AA234916 492 EST 3.2 down 0.00799<BR> rc\_AA235233\_at AA235233 493 EST 6.59 down 0.00755<BR> rc\_AA235288\_at AA235288 494 PTPL1-associated RhoGAP1 3.7 down 0.00643<BR> rc\_AA235310\_at AA235310 496 EST 37.86 down 0.00091<BR> rc\_AA235507\_at AA235507 498 golgi autoantigen, golgin subfamily a, 5 3.28 down 0.00249<BR> rc\_AA235618\_f\_at AA23518 499 EST 3.43 down 0.2127<BR> rc\_AA235765\_s\_at AA235765 501 KIAA2014 gene product 3.59 down 0.01148<BR> rc\_AA235811\_at AA235811 502 EST 3.64 down 0.01272<BR> rc\_AA235873\_s\_at AA235873 505 H factor (complement)-like 1, H factor 1 9.98 down 0.01667<BR> rc\_AA236230\_at AA236230 508 EST 5.28 down 0.01517<BR> rc\_AA236365\_s\_at AA236365 509 3-phosphoglycerate dehydrogenase 10.23 down 0.00562<BR> rc\_AA236401\_at AA236401 510 EST 16.71 down 0.00088<BR> rc\_AA236455\_r\_at AA236455 512 EST 15.71 down 0.00286<BR> rc\_AA236455\_s\_at AA236455 512 EST 11.35 down 0.02859<BR> rc\_AA236796\_s\_at AA236796 517 follistatin 8.74 down 0.00862<BR> rc\_AA236942\_at AA236942 519 EST 3.18 down 0<BR> rc\_AA236982\_at AA236982 520 sterol carrier protein 2 5.56 down 0.01542<BR> rc\_AA242766\_at AA242766 523 EST 3.58 down 0.0151<BR> rc\_AA243495\_at AA243495 528 lectin, mannose-binding, 1 4.23 down 0.00179<BR> rc\_AA243582\_at AA243582 529 hemoglobin, gamma A 7.15 down 0.0021<BR> rc\_AA243595\_s\_at AA243595 530 EST 3.11 down 0.008<BR> AA247453\_at AA247453 533 EST 3.09 down 0.0015<BR> rc\_AA250744\_at AA250744 536 EST 3.36 down 0.01137<BR> rc\_AA250775\_at AA250775 537 EST 4.52 down 0.01752<BR> rc\_AA251114\_at AA251114 539 prostate cancer overexpressed gene 1 6.6 down 0.00039<BR> rc\_AA251837\_at AA251837 547 EST 3.87 down 0.00782<BR> quinolinate phosphoribosyltransferase (nicotinate-<BR> rc\_AA252289\_at AA252289 552 nucleotide pyrophosphorylase (carboxylating)) 5.66 down 0.01389<BR> rc\_AA252365\_at AA252365 554 EST 3.9 down 0.01796<BR> rc\_AA253043\_at AA253043 559 DKFZP586I1419 protein 3.89 down 0.00145<BR> AA253129\_at AA253129 560 F-box protein FBL11 6.47 down 0.00001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA253216\_at AA253216 561 EST 28.18 down 0.00141<BR> rc\_AA253369\_s\_at AA253369 563 EST 15.59 down 0.00091<BR> rc\_AA253455\_s\_at AA253455 565 EST 3.05 down 0.00533<BR> rc\_AA253459\_at AA253459 566 EST 4.51 down 0.00419<BR> rc\_AA255546\_at



AA25546 569 EST 4 down 0.00301<BR> rc\_AA255624\_at AA255624 571 EST 4.06 down 0.00069<BR> rc\_AA255878\_at AA255878 572 KIAA0767 protein 3.96 down 0.00592<BR> rc\_AA255903\_at AA255903 573 CD39-like 4 5.67 down 0.01687<BR> rc\_AA256171\_at AA256171 575 EST 7.34 down 0.04562<BR> rc\_AA256341\_at AA256341 578 EST 7.37 down 0.00091<BR> rc\_AA256367\_s\_at AA256367 579 paraoxonase 3 70.33 down 0.00192<BR> rc\_AA256666\_at AA256666 583 EST 4.63 down 0.0018<BR> rc\_AA257057\_s\_at AA257057 586 EST 8.11 down 0.00379<BR> rc\_AA258308\_at AA258308 590 EST 5.4 down 0.00023<BR> rc\_AA258323\_at AA258323 591 EST 4.31 down 0.00046<BR> rc\_AA258350\_at AA258350 592 EST 5.08 down 0.00035<BR> rc\_AA258353\_at AA258353 593 EST 5.28 down 0.00193<BR> rc\_AA258567\_at AA258567 597 EST 6.92 down 0.00096<BR> rc\_AA258613\_at AA258613 598 EST 4.31 down 0.0344<BR> rc\_AA258813\_at AA258813 600 EST 4.63 down 0.02395<BR> rc\_AA259064\_at AA259064 602 EST 13.15 down 0.00001<BR> rc\_AA261954\_at AA261954 604 EST 7.69 down 0.00334<BR> rc\_AA262033\_s\_at AA262033 606 EST 4.41 down 0.00054<BR> rc\_AA262349\_at AA262349 607 EST 3.78 down 0.00043<BR> rc\_AA262766\_at AA262766 609 EST 5.66 down 0.3832<BR> rc\_AA279112\_at AA279112 622 EST 3.42 down 0.01444<BR> rc\_AA279533\_at AA279533 627 EST 5.01 down 0.04448<BR> AA279550\_at AA279550 628 Kruppel-like factor 4.06 down 0.00957<BR> rc\_AA279676\_s\_at AA279676 630 deoxyribonuclease I-like 3 23.35 down 0.00001<BR> rc\_AA279802\_at AA279802 631 EST 3.65 down 0.03366<BR> rc\_AA279937\_at AA279937 634 EST 3.38 down 0.02719 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA280130\_at AA280130 636 EST 4.12 down 0.00114<BR> spleen focus forming virus (SFFV) proviral<BR> rc\_AA280413\_s\_at AA280413 638 integration oncogene spi1 4.46 down 0.02063<BR> rc\_AA280791\_at AA280791 640 eukaryotic translation initiation factor 5 3.11 down 0.03339<BR> rc\_AA281440\_at AA281440 644 EST 6.43 down 0.01246<BR> rc\_AA281545\_at AA281545 645 EST 3.64 down 0.00002<BR> rc\_AA281591\_at AA281591 646 EST 3.23 down 0.00895<BR> AA281677\_at AA281677 648 DKFZP564M2423 protein 3.95 down 0.03606<BR> rc\_AA281770\_at AA281770 L649 seven in absentia (Drosophila) homolog 1 3.96 down 0.00094<BR> rc\_AA281796\_at AA281796 650 mannose-P-dolichol utilization defect 1 3.3 down 0.04108<BR> core-binding factor, runt domain, alpha subunit 2down?<BR> rc\_AA281930\_at AA281930 651 translocated to, 3 3.27 down 0.02329<BR> rc\_AA282061\_at AA282061 652 KIAA0962 protein 8.95 down 0.01033<BR> rc\_AA282089\_at AA282089 653 EST 4.93 down 0.00108<BR> rc\_AA282179\_at AA282179 655 EST 3.09 down 0.01693<BR> rc\_AA282238\_at AA282238 656 EST 3.47 down 0.00677<BR> rc\_AA282516\_at AA282516 660 7-dehydrocholesterol reductase 7.67 down 0.0008<BR> rc\_AA282886\_at AA282886 663 EST 3.57 down 0.00049<BR> rc\_AA282971\_at AA282971 665 EST 4.37 down 0.03822<BR> rc\_AA283758\_at AA283758 670 EST 3.67 down 0.04293<BR> AA284558\_at AA284558 674 Nck, Ash and phospholipase C binding protein 3.09 down 0.00027<BR> rc\_aa284721\_s\_at AA284721 677 EST 3.34 down 0.03296<BR> rc\_AA284795\_at AA284795 678 phosphatidylethanolamine N-methyltransferase 10.03 down 0.00019<BR> rc\_AA285053\_at AA285053 681 ST 6, 95 down 0.00125<BR> rc\_AA287122\_at AA287122 686 EST 3.66 down 0.00161<BR> rc\_AA287550\_f\_at AA287550 689 DKFZP434C171 protein 3.53 down 0.00217<BR> rc\_AA28756\_at AW287566 690 KIAA0187 gene product 9.07 down 0.00013<BR> rc\_AA291323\_at AA291323 699 BCL2-interacting killer (apoptosis-inducing) 9.15 down 0.00514<BR> rc\_AA291749\_s\_at AA291749 703 estrogen receptor 1 4.78 down 0.00059<BR> rc\_aa292086\_s\_at AA292086 705 EST 5 down 0.00161<BR> AA292158\_s\_at AA292158 706 EST 21.79 down 0.00031 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA292328\_at AA292328 707 activating transcription factor 5 17.51 down 0.00689<BR> rc\_AA292711\_at AA292711 711 EST 3 down 0.01053<BR> rc\_AA292773\_s\_at AA292773 713 collagen, type XVIII, alpha 1 7.44 down 0.00158<BR> rc\_AA293327\_at AA293327 716 isocitrate dehydrogenase 1 (NADP+), soluble 7.04 down 0.04377<BR> rc\_AA293485\_at AA293485 718 EST 3.36 down 0.02799<BR> AA298180\_at AA298180 726 EST 3.11 down 0.00747<BR> rc\_AA299632\_at

AA299632 728 EST 4.23 down 0.00371<BR> rc\_AA312946\_s\_at AA312946 731 EST 9.21 down 0.00106<BR> AA314457\_at AA314457 733 synaptonemal complex protein 3 4.86 down 0.0013<BR> rc\_AA338512\_at AA338512 742 EST 3.05 down 0.03427<BR> rc\_AA342301\_at AA342301 746 EST 3.89 down 0.00038<BR> rc\_AA342337\_at AA342337 747 EST 3.87 down 0.0069<BR> rc\_AA342446\_s\_at AA342446 748 insulin receptor 6.83 down 0.00412<BR> rc\_AA342771\_at AA342771 749 EST 5.33 down 0.00331<BR> rc\_AA343142\_at AA343142 751 EST 20.87 down 0.00003<BR> rc\_AA344866\_s\_at AA344866 752 complement component 8, gamma polypeptide 7.28 down 0.00206<BR> rc\_AA347674\_at AA347674 753 EST 10.59 down 0.03716<BR> rc\_AA347717\_at AA347717 754 EST 5.25 down 0.00207<BR> rc\_AA348284\_at AA348284 755 EST 4.54 down 0.00759<BR> rc\_AA348466\_s\_at AA348466 756 regulator of G-protein signalling 5 3.2 down 0.00571<BR> rc\_AA348485\_at AA348485 757 KIAA0438 gene product 4.01 down 0.04563<BR> fatty-acid-Coenzyme A ligase, long-chain 1, fatty-<BR> rc\_AA348922\_s\_at AA348922 758 acid-Coenzyme A ligase, long-chain 2 64.27 down 0.0002<BR> rc\_AA349836\_at AA349836 760 EST 3.01 down 0.00911<BR> KIAA0382 proteindown? leukemia-associated rho<BR> rc\_AA370359\_s\_at AA370359 767 guanine nucleotide exchange factor 9GEF) 4.82 down 0.01077<BR> AA376875\_at AA376875 770 monoamine oxidase A 3.8 down 0.02746<BR> rc\_AA377087\_at AA377087 771 EST 16.75 down 0.0002<BR> rc\_AA381125\_at AA381125 772 EST 15.48 down 0<BR> rc\_AA382975\_f\_at AA382975 773 EST 3.7 down 0.00131<BR> rc\_AA393825\_at AA393825 776 EST 3.62 down 0.0065 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> AA393961\_at AA393961 777 EST 3.7 down 0.01029<BR> AA397841\_at AA397841 780 EST 8.21 down 0<BR> rc\_AA397914\_at AA397914 783 EST 3.16 down 0.0033<BR> rc\_AA398102\_at AA398102 786 KIAA0429 gene product 6.22 down 0.00396<BR> rc\_AA398124\_s\_at AA398124 787 growth factor receptor-bound protein 14 7.82 down 0.00009<BR> rc\_AA398221\_at AA398221 790 calcium/calmodulin-dependent protein kinase 3.78 down .00019<BR> rc\_AA398257\_at AA398257 791 7-dehydrocholesterol reductase 4.43 down 0.04169<BR> rc\_AA398280\_at AA398280 792 EST 12.43 down 0.00134<BR> rc\_AA398386\_at AA398386 793 EST 5.71 down 0.00007<BR> rc\_AA398422\_i\_at AA398422 794 EST 3.94 down 0.00388<BR> rc\_AA398423\_at AA398423 795 EST 8.26 down 0.00063<BR> rc\_AA398445\_at AA398445 796 EST 4.28 down 0.01764<BR> rc\_AA398892\_at AA398892 800 similar to yeast BET3 (S. cerevisiae) 7.43 down 0.00038<BR> rc\_AA40030\_at AA40030 806 EST 3.98 down 0.00088<BR> rc\_AA400246\_at AA400246 810 mitogen-activated protein kinase-activated 3.09 down 0.00476<BR> rc\_AA400251\_at AA400251 811 EST 4.07 down 0.00032<BR> rc\_AA400258\_at AA400258 812 EST 11.89 down 0.00478<BR> rc\_AA400259\_at AA400259 813 EST 3.65 down 0.00476<BR> rc\_AA400471\_at AA400471 816 EST 5.45 down 0.0056<BR> rc\_AA400780\_at AA400780 818 EST 3.5 down 0.00107<BR> rc\_AA400831\_at AA400831 819 EST 3.49 down 0.00105<BR> rc\_AA400834\_f\_at AA400834 820 EST 4.73 down 0.01523<BR> rc\_AA400864\_at AA400864 821 down 7.51 down 0.02237<BR> rc\_AA400915\_at AA400915 823 EST 9.84 down 0.00351<BR> rc\_AA400934\_at AA400934 824 EST 4.98 down 0.02013<BR> rc\_AA400979\_at AA400979 825 calcitonin receptor0-like receptor activity modifying 6.65 down 0.01051<BR> rc\_AA401151\_at AA401151 827 lysozyme (renal amyloidosis) 3.01 down 0.0051<BR> rc\_AA401343\_at AA401343 828 EST 3.11 down 0.01929<BR> rc\_AA401376\_at AA401376 829 EST 3.97 down 0.00797<BR> rc\_AA401562\_s\_at AA401562 830 EST 50.45 down 0.00301<BR> AA402006\_at AA402006 834 EST 4.19 down 0.00094 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> AA402095\_s\_at AA402095 835 EST 3.12 down 0.01412<BR> rc\_AA402224\_at AA402224 836 growth arrest and DNA-damage-inducible, 14.41 down 0.0012<BR> rc\_AA402656\_at AA402656 841 EST 12.05 down 0.00001<BR> rc\_AA402799\_at AA402799 842 EST 11.81 down 0.00031<BR> AA404252\_at AA404252 848 lectin, mannose-binding, 1 16.15 down 0.0001<BR> rc\_AA404352\_at AA404352 850 EST 7 down 0.00059<BR> rc\_AA404500\_at AA404500 852 EST 4.16 down 0.01375<BR> rc\_AA405819\_at AA405819 865 KIAA0668 protein 8.59 down 0.02034<BR> rc\_AA405832\_at AA405832 866 EST 12.24 down 0.00441<BR> rc\_AA405907\_at

AA405907 867 EST 3.12 down 0<BR> rc\_aa406125\_s\_at AA406125 868 EST 4.95 down 0.01027<BR> rc\_AA406126\_at AA406126 869 EST 8.43 down 0.00569<BR> rc\_AA406231\_s\_at AA406231 873 KIAA0381 protein 4.46 down 0.04049<BR> AA406435\_s\_at AA406435 877 EST 3.24 down 0.00941<BR> rc\_AA410181\_at AA410181 881 EST 3 down 0.00268<BR> rc\_AA410255\_at AA410255 882\_s\_at at 7.56 down 0.00043<BR> rc\_AA410507\_at AA410507 884 EST 3.73 down 0.01703<BR> rc\_AA410523\_at AA410523 886 EST 6.37 down 0.03506<BR> rc\_AA411764\_at AA411764 891 similar to APOBEC1 4 down 0.01491<BR> rc\_AA412034\_at AA412034 894 EST 3.09 down 0.02309<BR> rc\_AA412063\_at AA412063 895 EST 8.26 down 0.0001<BR> rc\_AA412184\_at AA412184 898 EST 3.08 down 0.00012<BR> rc\_AA412481\_s\_at AA412481 902 EST 8.07 down 0.00014<BR> rc\_AA416723\_at AA416723 906 EST 3.57 down 0.01042<BR> rc\_AA416740\_s\_at AA416740 907 EST 3.08 down 0.01592<BR> rc\_AAE16873\_at AA416873 908 EST 7.82 down 0.00005<BR> sphingomyelin phosphodiesterase 1, acid<BR> rc\_AA416890\_s\_at AA416890 909 lysosomal (acid sphingomyelinase) 6.6 down 0.00112<BR> 5-methyltetrahydrofolate-homocysteine<BR> rc\_AA416936\_at AA416936 910 methyltransferase reductase 4.98 down 0.00632<BR> rc\_AA417046\_at AA417046 915 fatty-acid-Coenzyme A ligase, very long-chain 1 44 down 0 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA417078\_at AA417078 916 EST 4.1 down 0.00414<BR> rc\_AA417373\_at AA417373 917 EST 4.8 down 0.01342<BR> rc\_AA417375\_at AA417375 918 EST 4.21 down 0.00231<BR> AA418098\_at AA418098 920 cAMP responsive element binding protein-like 2 3.18 down 0.03824<BR> cytochrome P450, subfamily I (aromatic<BR> rc\_AA418907\_s\_at AA418907 922 compound-inducible), polypeptide 1 4.05 down 0.04276<BR> AA419507\_at AA419507 924 EST 5.58 down 0.00578<BR> rc\_AA419608\_at AA419608 925 EST 9.19 down 0.00005<BR> rc\_AA419622\_at AA419622 926 EST 4.62 down 0.00386<BR> rc\_AA421049\_at AA421049 927 activating transcription factor 5 44.41 down 0.00179<BR> rc\_AA421052\_at AA421052 929 branched chain alpha-ketoacid dehydrogenase 3.52 down 0.00869<BR> rc\_AA421244\_s\_at AA421244 932 SH3-domain binding protein 5 (BTK-associated) 4.32 down 0.007<BR> rc\_AA421561\_at AA421561 933 insulin-like growth factor 2 (somatomedin A) 9.98 down 0.00007<BR> AA424307\_at AA424307 944 EST 5.73 down 0.0074<BR> rc\_AA424672\_s\_at AA424672 946 dermatopontin 4.69 down 0.00843<BR> rc\_AA424798\_at AA424798 947 EST 17.45 down 0.00352<BR> rc\_AA424813\_at AA424813 948 EST 5.77 down 0.00503<BR> rc\_AA425294\_at AA425294 952 EST 10.61 down 0.00083<BR> rc\_AA425309\_at AA425309 953 nuclear factor I/B 4.9 down 0.00466<BR> rc\_AA425782\_at AA425782 956 KIAA0874 protein 5.52 down 0.03433<BR> rc\_AA425836\_at AA425836 957 EST 4.55 down 0.00035<BR> AA426156\_at AA426156 959 EST 3.67 down 0.00153<BR> AA426168\_at AA426168 960 KIAA0805 protein 3.73 down 0.01477<BR> AA426304\_s\_at AA426304 962 EST 6.61 down 0.01092<BR> rc\_AA426330\_at AA426330 963 N-acylsphingosine amidohydrolase (acid 4.24 down 0.00668<BR> rc\_AA426468\_at AA426468 966 EST 3.38 down 0.0099<BR> rc\_AA426609\_at AA426609 968 EST 6.28 down 0.01233<BR> rc\_AA427778\_at AA427778 978 EST 3.57 down 0.00368<BR> rc\_AA427783\_at AA427783 979 EST 4.37 down 0.0004<BR> rc\_AA427819\_at AA427819 980 midline 2 3.44 down 0.00063<BR> AA428006\_at AA428006 984 DKFZP564B167 protein 3.71 down 0.02325 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA428150\_at AA428150 985 EST 5.24 down 0.00167<BR> rc\_AA427325\_at AA428325 988 EST 8.36 down 0.00002<BR> rc\_AA428567\_at AA428567 989 EST 3.99 down 0.00788<BR> rc\_AA428607\_at AA428607 990 ribosomal protein S5 pseudogene 1 4.21 down 0.04305<BR> rc\_AA428863\_at AA428863 991 EST 3.5 down 0.01726<BR> rc\_AA428900\_at AA428900 992 EST 7.01 down 0.00037<BR> rc\_AA429038\_at AA429038 995 EST 3.29 down 0.00927<BR> rc\_AA429478\_at AA429478 998 EST 3.41 down 0.02599<BR> rc\_AA429904\_at AA429904 1005 EST 7.26 down 0.00524<BR> AA430011\_at AA430011 1006 EST 8.35 down 0.00729<BR> rc\_AA430026\_at AA430026 1007 EST 3.31 down 0.00786<BR> rc\_AA430028\_at AA430028 1008 EST 9.14 down 0.00246<BR> rc\_AA430044\_at AA430044 1010 EST 7.78 down 0.00124<BR> rc\_AA430047\_at AA430047 1011 EST 3.44 down

0.0016<BR> rc\_AA430108\_at AA430108 1013 EST 3.8 down 0.04484<BR> rc\_AA430666\_at  
 AA430666 1016 EST 5.12 down 0.00377<BR> rc\_AA431337\_at AA431337 1020 EST 6.26 down  
 0.00053<BR> rc\_AA431462\_at AA431462 1022 EST 4.45 down 0.00956<BR> rc\_AA431480\_s\_at  
 AA431480 1023 EST 4.3 down 0.0086<BR> rc\_AA431773\_at AA431773 1026 EST 7.61 down  
 0.00063<BR> rc\_AA432168\_at AA432168 1031 S-adenosylhomocysteine hydrolase-like 1 4.71 down  
 0.01377<BR> rc\_AA433946\_at AA433946 1033 EST 43.74 down 0.00005<BR> rc\_AA435591\_at  
 AA435591 1038 kinesin family member 3B 3.5 down 0.0001<BR> rc\_AA435753\_at AA435753 1045  
 EST 4.71 down 0.00078<BR> solute carrier family 25 (mitochondrial carrier;<BR> rc\_AA435777\_f\_at  
 AA435777 1047 citrate transporter), member 1 7.48 down 0.00613<BR> rc\_AA435824\_at AA435824  
 1048 EST 3.93 down 0.02764<BR> rc\_AA435985\_at AA435985 1049 EST 17.7 down 0<BR>  
 rc\_AA436489\_at AA436489 1053 EST 7.34 down 0.001<BR> rc\_AA436560\_at AA436560 1055  
 claudin 1 11.41 down 0.00756<BR> rc\_AA436690\_at AA436690 1057 EST 4.58 down 0.00948 Table  
 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq  
 ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA436880\_at AA436880 1058 EST  
 3.22 down 0.00699<BR> AA436926\_at AA436926 1059 EST 5.5 down 0.00984<BR>  
 rc\_AA437235\_s\_at AA437235 1060 EST 7.15 down 0.01455<BR> rc\_AA437265\_s\_at AA437265  
 1061 EST 4.39 down 0.00826<BR> rc\_AA437295\_at AA437295 1062 ribosomal protein L7a 4.35  
 down 0.00347<BR> rc\_AA441791\_at AA441791 1065 EST 3.58 down 0.00357<BR> AA442334\_at  
 AA442334 1069 EST 7.15 down 0.00018<BR> AA442342\_at AA442342 1070 EST 5.62 down  
 0.00052<BR> rc\_AA443272\_at AA443272 1074 EST 7.68 down 0.00869<BR> rc\_AA443658\_at  
 AA443658 1079 transmembrane 7 superfamily member 2 9.06 down 0.00048<BR> rc\_AA443756\_at  
 AA443756 1080 EST 5.05 down 0.00341<BR> rc\_AA443822\_at AA443822 1082 EST 5.46 down  
 0.02538<BR> rc\_AA443934\_at AA443934 1083 GTP-binding protein Rho7 3.09 down 0.00214<BR>  
 rc\_AA443936\_s\_at AA443936 1084 EST 22.96 down 0.00627<BR> rc\_AA443993\_at AA443993 1086  
 EST 3.21 down 0.02948<BR> rc\_AA446342\_at AA446342 1088 seven in absentia (Drosophila)  
 homolog 1 4.84 down 0.00015<BR> rc\_AA446587\_at AA446587 1091 EST 5.8 down 0.00012<BR>  
 rc\_AA446651\_at AA446651 1093 EST 3.14 down 0.01902<BR> rc\_AA446666\_at AA446666 1094  
 EST 4.03 down 0.02369<BR> UDP-N-acteylglucosamine pyrophosphorylase 1;<BR> rc\_AA447549\_at  
 AA447549 1101 Sperm associated antigen 2 6.37 down 0.02815<BR> rc\_AA447617\_at aa447617 1103  
 est 3.26 down 0.04687<BR> rc\_AA447740\_at AA447740 1106 EST 3.22 down 0.02518<BR>  
 rc\_AA447971\_at AA447971 1110 EST 8.08 down 0.00035<BR> rc\_AA447977\_s\_at AA447977 1111  
 EST 3.84 down 0.00045<BR> rc\_AA448002\_at AA448002 1113 putative type II membrane protein  
 10.05 down 0<BR> rc\_AA448282\_at AA448282 1115 EST 3.87 down 0.00217<BR> FXFD domain-  
 containing ion transport regulator 1<BR> rc\_AA448300\_at AA448300 1115 (phospholemman) 24.97  
 down 0.00001<BR> rc\_AA449267\_at AA449267 1120 EST 16.44 down 0.00926<BR>  
 rc\_AA449297\_at AA449297 1121 EST 3.78 down 0.00039 Table 6B. Down regulated in metastatic  
 cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold  
 Change Direction Pvalue<BR> rc\_AA448395\_at AA449306 1122 EST 5.01 down 0.0006<BR>  
 rc\_AA449327\_at AA449327 1123 EST 4.77 down 0.01248<BR> rc\_AA449448\_at AA449448 1125  
 EST 3.97 down 0.00103<BR> rc\_AA450114\_at AA450114 1131 EST 4.96 down 0.01238<BR>  
 rc\_AA450127\_at AA450127 1132 growth arrest and DNA-damage-inducible, beta 7.98 down  
 0.00078<BR> rc\_AA450281\_at AA450281 1134 EST 5.55 down 0.00004<BR> rc\_AA451836\_at  
 AA451836 1137 EST 4.9 down 0.01412<BR> rc\_AA451911\_at AA451911 1139 EST 3.44 down  
 0.00221<BR> rc\_AA452158\_at AA452158 1141 ras homolog gene family, member B 28.96 down  
 0.00064<BR> AA452454\_at AA452454 1144 EST 4.45 down 0.00179<BR> rc\_AA452549\_at  
 AA452549 1146 platelet-derived growth factor receptor, alpha 3.3 down 0.04155<BR>  
 rc\_AA452559\_s\_at AA452559 1147 EST 4.35 down 0.00804<BR> rc\_aa452598\_s\_at AA452598 1148  
 genethonin 1 5.49 down 0.00163<BR> rc\_AA452855\_at AA452855 1150 lectin, mannose-binding, 1  
 9.88 down 0.00428<BR> rc\_AA452860\_at AA452860 1151 EST 3.99 down 0.00831<BR>  
 rc\_AA452915\_at AA452915 1152 EST 3.13 down 0.00561<BR> rc\_AA453770\_s\_at AA453770 1157  
 EST 6.04 down 0.00524<BR> AA453917\_at AA453917 1159 EST 3.3 down 0.01896<BR>

rc\_AA453988\_at AA453988 1160 methionine adenosyltransferase I, alpha 54.29 down 0.00381<BR>  
rc\_AA454086\_f\_at AA454086 1161 UDP-glucose dehydrogenase 4.29 down 0.00981<BR>  
rc\_AA454159\_at AA454159 1162 EST 10.81 down 0.00132<BR> rc\_AA454170\_at AA454170 1163  
EST 3.11 down 0.03<BR> rc\_AA454177\_i\_at AA454177 1164 EST 10.3 down 0.0008<BR>  
rc\_AA454184\_at AA454184 1165 EST 3.96 down 0.04605<BR> rc\_AA454733\_s\_at AA454733 1169  
EST 5.61 down 0.01182<BR> rc\_AA455097\_i\_at AA455097 1172 EST 6.03 down 0.00419<BR>  
rc\_AA455367\_at AA455367 1176 DKFZP586F1018 protein 3.73 down 0.00202<BR> AA455403\_at  
AA455403 1177 EST 15.46 down 0.01547<BR> rc\_AA455865\_at AA455865 1180  
phosphatidylinositol glycan, class B 5.41 down 0.00004<BR> rc\_AA455806\_s\_at AA455896 1181  
glypican 1 3.46 down 0.00887<BR> rc\_AA455962\_at AA455962 1182 EST 3.1 down 0.03905 Table  
6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq  
ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA455987\_at AA455987 1183 EST  
5.36 down 0.00029<BR> butyrobetaine (gamma), 2-oxoglutarate<BR> rc\_AA455988\_at AA455988  
1184 dioxygenase (gamma-butyrobetaine hydroxylase) 15.54 down 0.00001<BR> rc\_AA456055\_at  
AA456055 1185 EST 5.16 down 0.00158<BR> rc\_AA456147\_at AA456147 1188 general transcription  
factor IIIA 4.23 down 0.00088<BR> rc\_AA456289\_at AA456289 1189 EST 15.31 down 0.00004<BR>  
rc\_AA456311\_s\_at AA456311 1190 EST 46.81 down 0.001<BR> rc\_AA456326\_at AA456326 1191  
EST 3.35 down 0.00489<BR> rc\_AA456589\_at AA456589 1194 EST 4.23 down 0.00102<BR>  
AA456687\_at AA456687 1197 EST 3.08 down 0.01189<BR> rc\_AA457377\_at AA457377 1201 EST  
3.1 down 0.00549<BR> rc\_AA458652\_at AA458652 1202 EST 8.26 down 0.00001<BR>  
rc\_AA458923\_at AA458923 1207 EST 3.36 down 0.00421<BR> rc\_AA458946\_at AA458946 1209  
EST 15.88 down 0.00004<BR> rc\_AA459256\_at AA459256 1212 lectin, mannose-binding, 1 3.01  
down 0.00094<BR> rc\_AA459293\_at AA459293 1213 EST 3.2 down 0.0001<BR> rc\_AA459389\_at  
AA459389 1216 tyrosylprotein sulfotransferase 2 3.72 down 0.02252<BR> rc\_AA459420\_at  
AA459420 1217 EST 7.25 down 0.0214<BR> rc\_AA459668\_at AA459668 1219 3-hydroxyisobutyryl-  
Coenzyme A hydrolase 7.62 down 0.00225<BR> rc\_aa459690\_s\_at AA459690 1221 EST 9.18 down  
0.00732<BR> solute carrier family 22 (extraneuronal<BR> rc\_AA460012\_at AA460012 1224  
monoamine transporter), member 3 4.27 down 0.04975<BR> AA460047\_at AA460047 1226 EST 3.33  
down 0.04011<BR> AA460128\_at AA460128 1227 similar to S. pombe din1+ 3.28 down  
0.01299<BR> rc\_AA460449\_at AA460449 1228 EST 7.77 down 0.00011<BR> rc\_AA460661\_at  
AA460661 1229 EST 7.02 down 0.00053<BR> rc\_AA460916\_at AA460916 1233 EST 3.69 down  
0.04841<BR> rc\_AA461057\_at AA461057 1234 nuclear localization signal deleted in 5.22 down  
0.00051<BR> rc\_AA461303\_at AA461303 1238 DKFZP586D 1519 protein 4.77 down 0.0438<BR>  
rc\_AA461444\_at AA461444 1239 EST 11.58 down 0.00167<BR> rc\_AA461458\_at AA461458 1241  
EST 3.37 down 0.02427 Table 6B. Down regulated in metastatic cancers versus normal sample set  
2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR>  
rc\_AA463194\_s\_at AA463194 1244 KIAA1037 protein 4.92 down 0.01866<BR> rc\_AA463195\_at  
AA463195 1245 EST 3.41 down 0.00413<BR> AA463311\_at AA463311 1248 EST 3.71 down  
0.04902<BR> rc\_AA463729\_at AA463729 1250 EST 4.07 down 0.00676<BR> rc\_AA463876\_at  
AA463876 1252 EST 3.31 down 0.00109<BR> rc\_AA463946\_at AA463946 1254 pigment epithelium-  
derived factor 3.38 down 0.0018<BR> rc\_AA464188\_s\_at AA464188 1256 EST 4.82 down  
0.03208<BR> rc\_AA464603\_at AA464603 1260 EST 3.26 down 0.0007<BR> rc\_AA465240\_at  
AA465240 1270 EST 4.03 down 0.0046<BR> rc\_AA470153\_at AA470153 1275 solute carrier family  
21 (organic anion 13.26 down 0.00315<BR> rc\_AA476324\_s\_at AA476324 1281 EST 55.22 down  
0.00132<BR> rc\_AA476346\_at AA476346 1283 EST 3.12 down 0.01067<BR> rc\_AA476352\_at  
AA476352 1284 EST 3.41 down 0.02233<BR> rc\_AA477119\_at AA477119 1289 EST 3.13 down  
0.0338<BR> AA477919\_at AA477919 1293 EST 4.69 down 0.00141<BR> AA477978\_s\_at  
AA477978 1294 short-chain dehydrogenase/reductase 1 8.53 down 0.01651<BR> rc\_AA478416\_at  
AA478416 1300 EST 4.04 down 0.00078<BR> rc\_AA478441\_at AA478441 1302 cathepsin F 5.07  
down 0.00752<BR> AA479132\_at AA479132 1309 EST 3.12 down 0.00876<BR> rc\_AA479148\_at  
AA479148 1311 EST 38.05 down 0<BR> rc\_AA479488\_at AA479488 1313 S-adenosylhomocysteine



hydrolase-like 1 4 down 0.0269<BR> rc\_AA479498\_at AA479498 1314 EST 5.78 down 0.01489<BR> rc\_AA479885\_at AA479885 1318 KIAA0843 protein 15.57 down 0.00024<BR> rc\_AA479968\_s\_at AA479968 1321 arylsulfatase A 9.01 down 0.00224<BR> rc\_AA480975\_at AA480975 1322 EST 8.95 down 0.00259<BR> rc\_AA480991\_s\_at AA480991 1323 EST 8.59 down 0.00156<BR> rc\_AA481432\_s\_at AA481432 1328 fibronectin 1 7.76 down 0.0061<BR> rc\_AA481526\_at AA481526 1329 EST 3.73 down 0.00002<BR> AA481670\_at AA481670 1330 retinal short-chain dehydrogenase/reductase 6.2 down 0.0078<BR> rc\_AA482594\_at AA482594 1337 EST 5.42 down 0.00387<BR> rc\_AA485089\_at AA485089 1341 EST 5.46 down 0.00044 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA485326\_at AA485326 1342 ATP-binding cassette, sub-family D (ALD), 3.08 down 0.00415<BR> rc\_AA485413\_at AA485413 1344 EST 4.54 down 0.00137<BR> aldehyde dehydrogenase 5 family, member A1<BR> rc\_AA486410\_at AA486410 1348 (succinate-semialdehyde dehydrogenase) 8.08 down 0.00485<BR> AA486511\_at AA486511 1349 EST 22.21 down 0.00113<BR> rc\_AA486567\_at AA486567 1350 EST 5 down 0.00002<BR> rc\_AA487161\_at AA487161 1353 ubiquitin 2 3.13 down 0.0023<BR> rc\_AA487603\_at AA487503 1356 EST 8.85 down 0.00012<BR> rc\_AA487606\_at AA487606 1358 EST 3.05 down 0.00291<BR> rc\_AA488843\_at AA488843 1362 comichon-like 8.58 down 0.02131<BR> rc\_AA489061\_at AA489061 1367 EST 3.49 down 0.00223<BR> rc\_AA489629\_at AA489629 1369 EST 8.08 down 0.00109<BR> rc\_AA489636\_at AA489636 1370 EST 10.7 down 0<BR> rc\_AA489798\_at AA489798 1373 hypothetical protein, estradiol-induced 875 down 0.00544<BR> rc\_AA490159\_at AA490159 1374 glucose-6-phosphatase, transport (glucose-6- 5.44 down 0<BR> rc\_AA490214\_at AA490214 1376 EST 3.12 down 0.02382<BR> rc\_AA490620\_at AA490620 1378 EST 4.77 down 0.00201<BR> rc\_AA490670\_at AA490670 1379 EST 9.96 down 0.00454<BR> UDP-N-acetylglucosamine-2-epimerase/N-<BR> AA490775\_AT AA490775 1380 acetylmannosamine kinase 5.34 down 0.0018<BR> rc\_AA490882\_s\_at AA490882 1381 EST 3.29 down 0.00319<BR> rc\_AA490890\_AT aa490890 1382 EST 3.02 down 0.00007<BR> rc\_AA491000\_AT aa491000 1385 EST 4.23 down 0.02305<BR> rc\_AA491001\_i\_at AA491001 1386 EST 8.52 down 0.01118<BR> rc\_AA491001\_f\_at AA491001 1386 EST 3.73 down 0.01957<BR> AA495758\_s\_at AA495758 1391 EST 3.94 down 0.00772<BR> rc\_AA495820\_at AA495820 1393 EST 3.98 down 0.00218<BR> rc\_AA496053\_at AA496053 1396 EST 3.28 down 0.00095<BR> AA496423\_at AA496423 1399 WW domain binding protein 2 3.52 down 0.01314<BR> rc\_AA496914\_at AA496914 1401 v-maf musculoaponeurotic fibrosarcoma (avian) 3.48 down 0.00361<BR> rc\_AA497052\_at AA497052 1408 DKFZP727G051 protein 7.28 down 0.01745 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA504492\_at AA504492 1414 tubulin, alpha, ubiquitous 4.21 down 0.00752<BR> AA50-5198\_at AA505198 1419 EST 3.41 down 0.0343<BR> rc\_AA521920\_at AA521290 1421 EST 4.53 down 0.0148<BR> rc\_AA521292\_at AA521292 1422 EST 8.58 down 0.00064<BR> rc\_AA521306\_at AA521306 1423 EST 4.27 down 0.00567<BR> UDP-N-acetylglucosamine-2-epimerase/N-<BR> rc\_AA598417\_AT AA598417 1426 acetylmannosamine kinase 8.56 down 0.01638<BR> rc\_AA598419\_s\_at AA598419 1427 translational inhibitor protein p14.5 23.6 down 0.00036<BR> rc\_AA598675\_at AA598675 1433 EST 3.25 down 0.03934<BR> rc\_AA598679\_at AA598679 1434 EST 5.37 down 0.00467<BR> rc\_AA598746\_at AA598746 1437 EST 3.8 down 0.02667<BR> rc\_AA598926\_at AA598926 1441 EST 3.7 down 0.00432<BR> rc\_AA599211\_at AA599211 1445 short-chain dehydrogenase/reductase 1 7.85 down 0.00911<BR> rc\_AA599234\_s\_at AA599234 1447 murine leukemia viral (bmi-1) oncogene homology 3.9 down 0.0068<BR> rc\_AA599472\_at AA599472 1451 succinate-CoA ligase, GDP-forming, beta subunit 5.07 down 0.00447<BR> rc\_AA599526\_at AA599526 1453 cartilage associated protein 3.02 down 0.00043<BR> rc\_AA599814\_at AA599814 1456 EST 12.37 down 0.00002<BR> rc\_AA599937\_s\_at AA599937 1458 insulin-like growth factor-binding protein 4 26.92 down 0.00094<BR> rc\_AA599954\_at AA599954 1459 cell cycle progression 8 protein 3.15 down 0.00021<BR> rc\_AA608546\_at AA608546 1463 EST 12.52 down 0.00003<BR> rc\_AA608671\_at AA608671 1466 EST 3.14 down 0.04543<BR> rc\_AA608729\_at AA608729 1468



EST 3.89 down 0.01757<BR> rc\_AA608751\_i\_at AA608751 1469 EST 5.76 down 0.01404<BR> rc\_AA608802\_at AA608802 1470 EST 6.95 down 0.00263<BR> rc\_AA608807\_s\_at AA608807 1471 inhibin, beta B (activin AB beta polypeptide) 4.05 down 0.005688<BR> rc\_AA608837\_at AA608837 1472 EST 6.2 down 0.00006<BR> rc\_AA609011\_at AA609011 1476 EST 3.94 down 0.0313<BR> rc\_AA609164\_at AA609164 1480 cytochrome b-561 6.8 down 0.02298<BR> rc\_AA609316\_at AA609316 1481 EGF-like-domain, multiple 5 7.97 down 0.00011<BR> rc\_AA609519\_at AA609519 1482 EST 8.13 down 0.00009<BR> rc\_AA609537\_s\_at AA609537 1483 hepatic leukemia factor 8.76 down 0.00018 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA609572\_at AA609572 1484 EST 3.02 down 0.01534<BR> rc\_AA609574\_at AA609574 1485 EST 5.03 down 0<BR> rc\_AA609576\_at AA609576 1486 EST 3.1 down 0.00266<BR> rc\_AA609773\_at AA609773 1489 EST 6.09 down 0.01103<BR> rc\_AA609774\_at AA609774 1490 EST 4.02 down 0.00424<BR> rc\_AA609934\_at AA609934 1493 EST 6.84 down 0.00048<BR> rc\_AA609996\_at AA609996 1495 EST 3.93 down 0.00988<BR> rc\_AA620343\_at AA620343 1500 EST 5.04 down 0.00407<BR> rc\_AA620556\_at AA620556 1505 EST 32.4 down 0.00353<BR> rc\_AA620667\_s\_at AA620667 1506 protein tyrosine phosphatase type IVA, member 1 5.92 down 0.00206<BR> rc\_AA620830\_at AA620830 1509 DKFZP564I122 protein 3.42 down 0.02421<BR> rc\_AA621131\_at AA621131 1513 EST 35.37 down 0<BR> rc\_AA621192\_at AA621192 1515 EST 5.39 down 0.0016<BR> rc\_AA621209\_at AA621209 1516 similar to Caenorhabditis elegans protein 6.34 down 0.00144<BR> rc\_AA621235\_at AA621235 1517 EST 3.44 down 0.0021<BR> rc\_AA621274\_i\_at AA621274 1519 EST 7.43 down 0.00065<BR> rc\_AA621430\_at AA621430 1525 doublecortin; lissencephaly, X-linked 3.09 down 0.00024<BR> rc\_AA621796\_at AA621796 1531 kinesin family member 3B 4.44 down 0.00032<BR> PDZ domain containing guanine nucleotide<BR> AB002311\_at AB002311 1535 exchange factor (GEF) 1; RA(Ras/Rap1A- 4.21 down 0.00476<BR> AB002328\_at AB002328 1536 calcineurin binding protein 1 5.55 down 0.00016<BR> AF000573\_ma1-at AF000573 143 homogentisate 1,2-dioxygenase (homogentisate 13.76 down 0.00002<BR> AF005039\_at AF005039 1548 secretory carrier membrane protein 3 3.42 down 0.04953<BR> solute carrier family 4, sodium bicarbonate<BR> AF007216\_at AF007216 1550 cotransporter, member 4 5.79 down 0.00005<BR> C01257\_at C01257 1554 EST 5.35 down 0.00608<BR> C01286\_s\_at C01286 1555 integral membrane protein 2B 4.11 down 0.00292<BR> C01409\_s\_at C01409 1556 EST 4.41 down 0.01725<BR> C01686\_at C01686 1557 EST 3.01 down 0.00048<BR> C02099\_s\_at C02099 1560 CGI-131 protein 5.85 down 0.02377<BR> C02460\_at c02460 1562 EST 3.64 down 0.02705 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_C14963\_s\_at C14963 1572 nicotinamide nucleotide transhydrogenase 3.9 down 0.0044<BR> C15871\_at C15871 1575 EST 3.26 down 0.00046<BR> C16420\_s\_at C16420 1576 EST 5.95 down 0.00119<BR> rc\_C20653\_at C20653 1578 EST 10.59 down 0.00001<BR> rc\_C20810-at C20810 1579 EST 5.17 down 0.00614<BR> rc\_C20911\_at C20911 1580 antithrombin III 6.56 down 0.00175<BR> rc\_C20974\_at C20974 1581 Vanin 1 6.66 down 0.00272<BR> rc\_C21130\_at C21130 1583 EST 8.79 down 0.00008<BR> rc\_C21238\_at C21238 1584 EST 4.54 down 0.02074<BR> cytochrome P450, subfamily IIIA (niphedipine<BR> D00003\_s\_at D00003 1586 oxidase), polypeptide 3 22.05 down 0.00059<BR> cytochrome P450, subfamily IIIa (niphedipine<BR> D00003\_at D00003 1586 oxidase), polypeptide 3 9.46 down 0.00001<BR> D00097\_s\_at D00097 1588 amyloid P component, serum 16.72 down 0.0098<BR> cytochrome P450, subfamily IIIA (niphedipine<BR> oxidase), polypeptide 3, cytochrome p450,<BR> subfamily IIIA (niphedipine oxidase), polypeptide<BR> D00408\_s\_at D00408 1589 5, cytochrome P450, subfamily IIIA, polypeptide 7 11.1 dwn 0<BR> D00632\_at D00632 1591 glutathione peroxidase 3 (plasma) 6.55 down 0.00121<BR> D00723\_at D00723 1592 glycine cleavage system protein H (aminomethyl 4.18 down 0.00543<BR> D10040\_at D10040 1593 fatty-acid-Coenzyme A ligase, long-chain 2 20.51 down 0<BR> acetyl-coenzyme A cactyltransferase 1<BR> D10511\_at D10511 1594 (acetoacetyl Coenzyme A thiolase) 10.68 down 0.0002<BR> rc\_D11756)\_f\_at D11756 1596 EST 5.49 down 0.01272<BR> rc\_D11802\_at D11802 1597 angiotensinogen 5.65 down

0.00009<BR> rc\_D11835\_at D11835 1598 low density lipoprotein receptor (familial 21.76 down  
0.00307<BR> rc\_D1881\_at D11881 1599 KIAA0962 protein 4.37 down 0.01627<BR>  
phosphodiesterase 1/nucleotide pyrophosphatase<BR> D12485\_at D12485 1600 1 (homologous to ouse  
LY-41 antigen) 4.57 down 0.00008 Table 6B. Down regulated in metastatic cancers versus normal  
sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction  
Pvalue<BR> cytochrome P450, subfamily IVF, polypeptide<BR> 2, cytochrome p450, subfamily IVF,  
polypeptide 3<BR> D12620-s\_at D1262 1601 (leukotriene B4 omega hydroxylase) 35.09 down  
0.00015<BR> cytochrom P450, subfamily IVF, polypeptide<BR> 2, cytochrome P450, subfamily IVF  
polypeptide 3<BR> D12620\_s\_at D12620 1601 (leukotriene B4 omega hydroxylase) 13.45 down  
0<BR> D13243\_s\_at D13243 1602 pyruvate kinase, liver and RBC 20.22 down 0<BR> D13643\_at  
D13643 1609 KIAA0018 gene product 10./84 down 0.00058<BR> D13705\_s\_at D13705 1610  
cytochrome P450, subfamily IVAm, polypeptide 11 3.7 down 0.00038<BR> D13814\_s\_at D13814  
1611 angiotensin receptor 1, angiotensin receptor 1B 3.12 down 0.00101<BR> D14012\_s\_at D14012  
1612 HGF activator 12.75 down 0.0035<BR> D14664\_at D14664 1616 KIAA0022 gene product 8.98  
down 0.00011<BR> D14695\_at D14695 1618 KIAA025 gene product: MMS-inducible gene 6.48 down  
0<BR> acetyl-Coenzyme A acyltransferase 2<BR> D16294\_at D16294 1619 (mitochondrial 3-oxoacyl-  
Coenzyme A thiolase) 4.81 down 0.03921<BR> D16350\_at D16350 1620 SA (rat hypertension-  
associated) homology 383 down 0.00117<BR> hydroxyacyl-Coenzyme A dehydrogenase/3-<BR>  
ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme<BR> D16481\_at D16481 1621 A hydratase  
(trifunctional protein), beta subunit 3.18 down 0.00695<BR> D16626\_at D16626 1622 histidine  
ammonia-lyase 22.66 down 0<BR> D16626\_at D16626 1622 histidine ammonia-lyase 925 down  
0.00025<BR> rc\_D20350\_at D20350 1624 EST 13.97 down 0.00057<BR> D31117\_at D31117 1640  
ribosome binding protein 1 (dog 180kD homolog)\_ 5.3 down 0.02749<BR> D31225\_at D31225 1641  
EST 3.17 down 0.01073<BR> D31289\_at D31289 1642 EST 4.16 down 0.02166<BR> D31381\_at  
D31381 1644 dynei, axonemal, light polypeptide 4 4.97 down 0.01806<BR> D31628\_s\_at D31628  
1646 4-hydroxyphenylpyruvate dioxygenase 50.48 down 0.00002<BR> D31716\_at D31716 1647 basic  
transcription element binding protein 1 5.35 down 0.00086<BR> D31815\_at D31815 1648 regucalcin  
(senescence marker protein-30) 10.55 down 0.00037<BR> d31887\_at D31887 1649 KIAA0062 protein  
4.26 down 0.00101<BR> D37931\_at D37931 1650 ribonuclease, RNase A family, 4 5.81 down 0.00836  
Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank  
Seq ID Known Gene Name Fold Change Direction Pvalue<BR> inter-alpha (globulin)\_ inhibitor H4  
(plasma<BR> D38535\_at D38535 1654 Kallikrein-sensitive glycoprotein) 13.2 down 0.01165<BR>  
rc\_D45529\_at D45529 1662 EST 3.82 down 0.00193<BR> rc\_D45556\_at D45556 1663 EST 4.83  
down 0.01044<BR> rc-D45714\_at D45714 1664 EST 5.64 down 0.00384<BR> D49357\_at D49357  
1665 methionine adenosyltransferase I, alpha 11.28 down 0.00331<BR> D49387-at D49387 1666  
NADP dependent leukotriene b4 12- 8.17 down 0.00972<BR> D49742\_at D49742 1668 hyaluronan-  
binding protein 2 18.13 down 0.00012<BR> rc\_D51199\_at D51199 1677 EST 5.05 down 0.00192<BR>  
rc\_D51279\_s-at D51279 1679 ovarian granulosa cell protein (13kD) 5.88 down 0.01271<BR>  
rc\_D52097\_s\_at D52097 1682 prostatic binding protein 8.1 down 0.00141<BR> D57823\_at D57823  
1690 Sec23 (S. cerevisiae) homolog A 4.43 down 0<BR> D58231\_s\_at D58231 1692 ubiquitin-like 3  
3.07 down 0.0002<BR> rc\_D59344\_s\_at D59344 1695 EST 3.34 down 0.01337<BR> rc\_D59554\_f-at  
D59544 1698 EST 6.7 down 0<BR> rc\_D59714\_s\_at D59714 1700 mitogen inducible 2 17.62 down  
0.00014<BR> rc\_D60670\_at D60670 1702 EST 3.73 down 0.00382<BR> rc\_D60769\_s\_at D60769  
1703 KIAA0096 protein 4.31 down 0.00142<BR> rc\_D60856\_f\_at D60856 1705 UDP-glucose  
dehydrogenase 6.45 down 0.01222<BR> D61991\_at D61991 1706 EST 4.84 down 0.00005<BR>  
D62103\_s\_at D62103 1707 EST 4.11 down 0.0263<BR> rc\_D62518\_at D62518 1708 EST 17.49 down  
0.00017<BR> D63160\_at D63160 1709 ficolin (collagen/fibrinogen domain-containing 4.01 down  
0.00391<BR> D78011\_at D78011 1717 dihydropyrimidinase 21.37 down 0.00003<BR> D79276 at  
D79276 1722 succinate-CoA ligase, GDP-forming, beta subunit 6.8 down 0.00047<BR> D79687\_at  
D79687 1723 KIAA1053 protein 5.06 down 0.00047<BR> rc\_D80050\_at D80050 1726 EST 4.64 down  
0.01001<BR> rc\_D80217\_f-at D80217 1727 H91620p protein 3.61 down 0.01973<BR> rc\_D80218-

f\_at D80218 1728 brain acid-souble protein 1 3.83 down 0.0137<BR> rc\_D80312\_f\_at D80312 1730 EST 3.74 down 0.01909<BR> rc\_D80408\_at D80408 1731 EST 3.36 down 0.00102 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_D80905\_at D80905 1735 EST 3.59 down 0.0007<BR> D82061\_at D82061 1741 Ke6 genem, mouse, human homoog of 6.1 down 0.00104<BR> D82422\_at D82422 1745 ferroportin 1'; iron regulated gene 1 6.01 down 0.02351<BR> D85181-at D85181 1750 sterol-C5-desaturase (fungal ERG3, delta-5- 9.56 down 0.00005<BR> D86062\_s\_at D86062 1752 ES1 (zebrafish) protein, human homolog of 3.63 down 0.0001<BR> D87075\_at D87075 1760 solute carrier family 23 (nucleobase transporters), 4.15 down 0.00067<BR> D87436\_at D87436 1761 KIAA0249 gene product 5.49 down 0.00333<BR> D87449\_at D87449 1762 KIAA0260 protein 4.58 down 0.00026<BR> D87466\_at D87466 1763 KIAA0276 protein 4.83 down 0.0007<BR> D90042\_at D90042 1767 N-acetyltransferase 2 (arylamine N- 7.06 down 0<BR> D90282\_at D90282 1769 carbamoyl-phosphate synthetase 1, mitochondrial 27.29 down 0.00002<BR> rc\_F02028\_at F02028 1774 EST 23.48 down 0.00465<BR> rc\_F02094\_at F02094 1775 ecotropic viral integration site 5 3.41 down 0.0495<BR> rc\_F02245\_at F0-2245 1776 monoamine oxidase A 3.9 down 0.02943<BR> rc\_F02345\_at F02345 1779 EST 3.9 down 0.0033<BR> rc\_F03200\_at F03200 1783 EST 3.75 down 0.01805<BR> matrix metalloproteinase 2 (gelatinase A, 72kD<BR> rc\_F03969\_at F03969 1785 gelatinase, 72kD type IV collagenase) 7.87 down 0.00014<BR> rc\_F04335\_at F04335 1787 EST 3.16 down 0.0058<BR> rc\_F04611\_at F04611 1792 EST 23.96 down 0.00018<BR> rc\_F04944\_s\_at F04944 1795 acyl-Coenzyme A oxidase 4.01 down 0.00242<BR> rc\_F088170-at F08817 1796 EST 8.29 down 0.0077<BR> rc\_F08941\_at F08941 1798 EST 3.48 dosn 0.00428<BR> rc\_F09058\_at F09058 1799 EST 3.6 down 0.00595<BR> rc\_F09350\_at F09350 1801 EST 4.79 down 0.00088<BR> rc\_F09353\_at F09353 1802 solute carrier family 5 (inositol transporters), 3.3 down 0.02841<BR> core-binding facotr, runt domain, alpha subunit 2 ;<BR> rc\_F09578\_at F09578 1804 translocated to, 3 4.66 down 0.04463<BR> rc\_F09979\_at F9979 1809 EST 4.36 down 0.02555<BR> rc\_F10182\_s\_at F10182 1812 hepsin (transmembrane protease, serine 1) 58.92 down 0.00837<BR> rc\_F10276\_s\_at F10276 1814 dual specificity phosphatase 6 8.13 down 0.0001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_F10466\_at F10466 1820 EST 5.32 down 0.02494<BR> rc\_F10640\_at F10640 1821 EST 3.58 down 0.00152<BR> rc\_F10874\_f\_at F10874 1823 EST 4.19 down 0.00025<BR> rc\_F10875\_at F10875 1824 EST 5.09 down 0.0004<BR> rc\_F13702\_at F13702 1826 EST 6.01 down 0.00064<BR> rc\_F13782\_s\_at F13782 1827 LIM binding domain 2 4.17 down 0.00109<BR> TEK tyrosine kinase, endothelial (venous<BR> rc\_H02848-s-at H02848 1831 malformations, multiple cutaneous and mucosal) 3.47 down 0.089<BR> rc\_H02855\_at H02855 1832 EST 5.96 down 0.00458<BR> rc\_H03348\_at H03348 1833 claudin 1 5.77 down 0.0001<BR> rc\_H03945\_at H03945 1835 EST 4.94 down 0.02603<BR> rc\_H04142\_f\_at H04142 1836 EST 3.57 down 0.01906<BR> rc\_H04242\_at H04242: 1837 RAB5B, member RAS oncogene family 3.27 down 0.04826<BR> H04854\_at H04854 1842 interleukin 1 receptor accessory protein 6.58 down 0.00007<BR> rc\_H05072\_at H05072 1843 EST 3.12 down 0.01248<BR> rc\_H05974\_s\_at H05974 1850 EST 6.28 down 0.0549<BR> rc\_H05985\_at H05985 1851 hypothetical protein 6.43 down 0.04887<BR> rcH06063\_s\_at H06063 1852 chondrotin sulfate proteoglycan 3 (neurocan) 3.15 down 0.00599<BR> rc\_H06144\_at H06144 1853 EST 3.1 down 0.00745<BR> rc\_H06166\_at H06166 1854 EST 3.31 down 0.03778<BR> rc\_H06935\_s\_at H06935 1855 electron-transferring-flavoprotein dehydrogenase 6.82 down 0.00105<BR> rc\_H08054\_at H08054 1857 EST 4.2 down 0.0009<BR> rc\_H08102\_at H08102 1858 breast cell glutaminase 27.77 down 0.00032<BR> rc\_H09167\_at H09167 1860 KIAA0195 gene product 3.31 down 0.00313<BR> rc\_H09353\_at H09353 1866 EST 23.06 down 0.00094<BR> H09364\_s\_at H09364 1867 succinats dehydrogenase complex, subunit A, 5.74 down 0.03125<BR> rc\_H09594-at H09594 1868 EST 3.12 down 0.00231<BR> rc\_H09959\_s\_at H09959 1869 choline kinase 3.25 down 0.00225<BR> H10482\_at H10482 1870 EST 3.19 down 0.01611<BR> rc\_H10661\_at H10661 1871 EST 4.54 down 0.00276 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change

Direction Pvalue<BR> methylenetetrahydrofolate dehydrogenase<BR> (NADP+ dependent), methenyltetrahydrofolate<BR> rc\_H10779\_s\_at H10779 1872 cyclohydrolase, formyltetrahydrofolate synthetase 9.73 down 0.00035<BR> rc\_H11274-at H11274 1874 EST 4.13 down 0.01478<BR> glycine dehydrogenase (decarboxylating; glycine<BR> rc\_H11739\_s\_at H11739 1876 decarboxylase, glycine cleavage system protein 10.33 down 0.00023<BR> rc\_H11746\_at H11746 1877 EST 3.92 down 0.00012<BR> rc\_H12257\_at H12257 1879 EST 3.19 down 0.0069<BR> rc\_H12593\_at H12593 1880 zinc-finger protein 265 10.72 down 0.0056<BR> rc\_H13696\_at H13696 1882 EST 3.46 down 0.01796<BR> rc\_H14372\_s\_at H14372 1883 ATP binding cassette, sub-family A (ABC1), 5.16 down 0.00012<BR> rc\_H16768\_at H16768 1887 EST 3.72 down 0.00688<BR> rc\_H18950\_at H18950 1892 EST 3.85 down 0.00162<BR> rc\_H18997\_at H18997 1893 F-box protein 21 3.87 down 0.00611<BR> rc\_H19504\_f\_at H19504 1895 EST 3.13 down 0.04948<BR> rc\_H20543\_at H20543 1897 DKFZP586B1621 protein 31.03 down 0.00074<BR> rc\_H25124\_at H25124 1903 EST 3.65 down 0.00004<BR> rc\_H25551\_at H25551 1904 EST 3.54 down 0.00366<BR> rc\_H25836\_at H25836 1905 tumor necrosis factor (ligand) superfamily, 3.3 down 0.03125<BR> rc\_H26417\_at H26417 1906 EST 3.22 down 0.03672<BR> rc\_H26763\_at H26763 1907 EST 3.39 down 0.04188<BR> rc\_H27330\_at H27330 1909 EST 3.2 down 0.00067<BR> rc\_H27442\_s\_at H27442 1910 erythrocyte membrane protein band 7.2 6.81 down 0.00083<BR> rc\_H29568\_at H29568 1914 EST 11.45 down 0.00058<BR> rc\_H30270\_at H30270 1915 EST 17.09 down 0.00001<BR> rc\_H38246\_s\_at H38246 1917 EST 9.25 down 0.00157<BR> rc\_H39119\_at H39119 1919 EST 3.06 down 0.03349<BR> rc\_H40149\_at H4019 1921 KIAA0937 rotein 4.59 down 0.00112<BR> rc\_H40424\_s\_at H40424 1922 butyrate response factor 1 (EGF-response factor 3.56 down 0.04066<BR> rc\_H40534\_at H40534 1923 EST 3.18 down 0.01381<BR> rc\_H41084\_at H41084 1924 EST 6.31 down 0.0227 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_H41280\_at H41280 1925 EST 3.68 down 0.00455<BR> rc\_H42053\_s\_at H42053 1927 EST 3.49 down 0.01057<BR> rc\_H46001\_at H46001 1931 EST 5.03 down 0.00563<BR> H46990\_at H46990 1993 cytochrome P450, subfamily IIE (ethanol- 3.2 down 0.00095<BR> rc\_H47391\_at H47391 1935 EST 3.1 down 0.03807<BR> rc\_H47838\_at H47838 1936 carboxypeptidase B2 (plasma) 16.74 down 0.00002<BR> rc\_H49415\_at H49415 1938 EST 3.72 down 0.005<BR> rc\_H51340\_at H51340 1941 EST 3.73 down 0.02643<BR> rc\_H54285\_s\_at H54285 1947 EST 5.14 down 0.00426<BR> rc\_H55759\_at H55759 1949 EST 11.52 down 0.00034<BR> 4-nitrophenylphosphatase domain and non-<BR> rc\_H56584\_at H56584 1951 neuronal SNAP25-like 1 9.5 down 0<BR> rc\_H57060-s\_at H57060 1954 EST 30.98 down 0.01687<BR> rc\_H57166\_at H57166 1955 EST 60.76 down 0.00007<BR> rc\_H57816\_at H57816 1957 EST 4.41 down 0.00206<BR> protein phosphatase 2 (formerly 2A), regulatory<BR> rc\_H57850\_at H57850 1958 subunit A (PR 65), beta isoform 3.02 down 0.00123<BR> rc\_H58673\_at H58673 1959 EST 14.85 down 0.00005<BR> rc\_h58692\_s\_at H58692 1960 formyltetrahydrofolate dehydrogenase 81.41 down 0<BR> rc\_H59136-at 59136 1962 EST 8.64 down 0.00013<BR> rc\_H59141\_at H59141 1963 EST 3.12 down 0.00293<BR> rc\_H60595\_s\_at H60-595 1966 progesterone binding protein 15.8 down 0.01078<BR> rc\_H61295\_s\_at H61295 1968 CD4 antigen (p55) 10.71 down 0.00925<BR> rc\_H62838\_at H62838 1971 EST 3.09 down 0.03201<BR> rc\_H63251\_at H63251 1972 KIAA0606 protein; SCN Circadian Oscillatory 3.27 down 0.02455<BR> rc\_H65650\_at H65650 1976 EST 3.88 down 0.0083<BR> rc\_H66367\_at H66367 1977 EST 6.68 down 0.0001<BR> rc\_H66840-at H66840 1978 EST 3.67 down 0.0143<BR> rc\_H67094\_at H67094 1979 EST 3.24 down 0.00075<BR> rc\_H67840\_at H67840 1980 EST 3.1 down 0.00528<BR> rc\_H68097\_at H68097 1982 EST 3.83 down 0.00797 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> H68953\_at H68953 1985 tranferrin 6.4 down 0.00132<BR> rc\_H69138\_at H69138 1986 v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene 6.76 down 0.00142<BR> rc\_H69565\_at H69565 187 EST 4.11 down 0.00002<BR> rc\_H70554\_at H70554 1989 EST 10.99 down 0<BR> rc\_H71169\_at H71169 1992 putative protein similar to nessy (Drosophila) 4 down 0.00709<BR> glucan (1,4-alpha-), branching enzyme 1<BR> rc\_H71861\_s\_at H71861 1993 (glycogen branching enzyme, Andersen disease, 5.97 down 0.00007<BR> rc\_H73535-s\_at H73535 1996 EST 6.89

down 0.00202<BR> rc\_H74317\_s\_at H74317 1997 apolipoprotein-A-II 45.09 down 0.01982<BR>  
 rc\_H77597\_f\_at H77597 2000 metallothionein 1H 16.03 down 0.00675<BR> H78628\_at H78628 2003  
 EST 4.98 down 0.00729<BR> rc\_H79820\_at H79820 2004 EST 3.25 down 0.01466<BR>  
 rc\_H80901\_s\_at H80901 2005 ficolin (collagen/fibrinogen domain-containing) 3 50.61 down  
 0.00262<BR> rc\_H81070\_f\_at H81070 2006 RNA helicase-related protein 25.74 down 0.00126<BR>  
 rc\_H82966\_s\_at H82966 2011 apolipoprotein B (including Ag(x) antigen) 3.42 down 0.00769<BR>  
 rc\_H83109-f\_at H83109 2012 EST 16.55 down 0.00001<BR> rc\_H83442\_s\_at H83442 2013  
 catechol-O-methyltransferase 3.99 down 0.00594<BR> rc\_H83451\_at H83451 2014 EST 3.35 down  
 0.00498<BR> rc\_H87144\_at H87144 2016 EST 3.41 down 0.00387<BR> rc\_H87765\_at H87765 2017  
 KIAA0626 gene product 3.86 down 0.00131<BR> H88033\_s\_at H88033 2019 KIAA0733 protein 4.42  
 down 0.02032<BR> rc\_H88359\_s\_at H88359 2020 nuclear factor (erythroid-derived 2)-like 2 5.16  
 down 0.01253<BR> rc\_H88675\_at H88675 2022 EST 5.63 down 0.00554<BR> rc\_H89514\_s\_at  
 H89514 2023 protein kinase, cAMP-dependent, catalytic, alpha 3.44 down 0.00435<BR> rc\_H99893\_at  
 H99893 2025 EST 3.17 down 0.00658<BR> rc\_H99980\_at H99980 226 protein phosphatase 1,  
 regulatory (inhibitor) 31.13 down 0.00006<BR> rc\_H90417\_s\_at H90417 2028 EST 4.17 down  
 0.015<BR> rc\_H91325-s\_at H91325 2029 aldolase B, fructose-bisphosphate 45.85 down 0.00505<BR>  
 rc\_H91456\_s\_at H91456 2030 nuclear receptor subfamily 1, group H, member 4 4.9 down  
 0.00255<BR> phosphorylase, glycogen; liver (Hers disease,<BR> rc\_H91680-s\_at H91680 2032  
 glycogen storage disease type VI) 4.15 down 0.00746 Table 6B. Down regulated in metastatic cancers  
 versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change  
 Direction Pvalue<BR> glutamate-cysteine ligase (gamma-<BR> rc\_H93053\_s\_at H93053 2034  
 glutamylcysteine synthetase), catalytic (72.8kD) 5.06 down 0.01029<BR> rc\_H93246\_s\_at H93246  
 2035 EST 15.3 down 0.0023<BR> rc\_H93381\_at H93381 2036 EST 24.23 down 0<BR> rc\_H3562\_at  
 H93562 2038 proline synthetase co-transcribed (bacterial 3.17 down 0.0113<BR> 3-hydroxy-3-  
 methylglutaryl-Coenzyme A synthase<BR> rc\_H94247\_s\_at H94247 2041 2 (mitochondrial) 9.49  
 down 0.02373<BR> rc\_H94475\_s\_at H94475 2043 alpha-2-plasmin inhibitor 40.92 down  
 0.00271<BR> rc\_H94648\_at H94648 2044 EST 4.77 down 0.00266<BR> rc\_H94666\_at H94666 2045  
 alpha-1-B glycoprotein 47.03 down 0.01158<BR> rc\_H95358\_at H95358 2049 EST 3.17 down  
 0.00182<BR> rc\_H95569\_i\_at H95569 2051 DKFZP586A0522 protein 28.48 down 0.00139<BR>  
 rc\_H95978\_at H95978 2052 EST 8.55 down 0.00046<BR> rc\_H96614\_at H96614 2054 EST 4.02  
 down 0.01565<BR> rc\_H97868\_at H97868 2064 EST 3.86 down 0.00362<BR> rc\_H97986\_at H97986  
 2065 EST 3.86 down 0.01534<BR> rc\_H98071\_at H98071 2066 EST 4.66 down 0.03722<BR>  
 rc\_H98083\_at H98083 2067 EST 5.09 down 0.00025<BR> rc\_H98771\_i\_at H98771 2069  
 BCL2/adenovirus E1B 19kD-interacting protein 8 down 0.0018<BR> rc\_H98822\_at H98822 2070 EST  
 3.31 down 0.00174<BR> rc\_H98910\_s\_at H98910 2071 EST 4.38 down 0.00548<BR> rc\_H98977\_at  
 H98977 2073 EST 3.57 down 0.00298<BR> rc\_H99393\_s\_at H99393 2076 endothelin receptor type B  
 3.43 down 0.00093<BR> rc\_H99727\_at H99727 2080 adipose differentiation-related protein;  
 adipophilin 5.83 down 0.04346<BR> rc\_H99935\_s\_at H99935 2085 interleukin 6 signal transducer  
 (gp130, oncostatin 3.59 down 0.00366 Table 6B. Down regulated in metastatic cancers versus normal  
 sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction  
 Pvalue<BR> J02843\_at J02843 2088 cytochrome P450, subfamily IIE (ethanol- 22.58 down  
 0.00935<BR> J002888\_at J02888 2089 NAD(P)H menadione oxidoreductase 2, dioxin- 3.15 down  
 0.02385<BR> J02943\_at J02943 2090 corticosteroid binding globulin 18.98 down 0.00087<BR>  
 J03242\_s\_at J03242 2092 insulin-like growth factor 2 (somatomedin A) 4.01 down 0.00042<BR>  
 J03507\_at J03507 2095 complement component 7 3.77 down 0.00184<BR> J03764\_at J03764 2097  
 plasminogen activator inhibitor, type I 5.6 down 0.02196<BR> protein phosphatase 2 (formerly 2A),  
 catalytic<BR> J03805\_s\_at J03805 2098 subunit, beta isoform 3.87 down 0.0116<BR> J03810\_at  
 J03810 2099 solute carrier family 2 (facilitated glucose 21.99 down 0.00004<BR> J03910\_ma1\_at  
 J03910 2101 EST 12.42 down 0.01167<BR> methylenetetrahydrofolate dehydrogenase<BR> (NADP+  
 dependent), methylenetetrahydrofolate<BR> J04031\_at J04031 2103 cyclohydrolase,  
 formyltetrahydrofolate synthetase 3.4 down 0.00786<BR> J04056\_at J04056 2104 carbonyl reductase 1



5.19 down 0.00001<BR> J04080\_at J04080 2105 complement component 1, s subcomponent 5.48 down 0.0239<BR> J04093\_s\_at J04093 2106 UDP glycosyltransferase 1 18.92 down 0 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> J04093\_s\_at J04093 2106 UDP glycosyltransferase 1 18.92 down 0<BR> cytochrome P450, subfamily IIIA (niphedipine<BR> J04449\_at J04449 2110 oxidase), polypeptide 3 5.25 down 0.01583<BR> J04615\_at J04615 2112 SNRPN upstream reading frame 3.14 down 0.02928<BR> syndecan 2 (heparan sulfate proteoglycan 1, cell<BR> J04621\_at J04621 2113 surface-associated fibroglycan) 3.38 down 0.00275<BR> cytochrome P450, subfamily IIIA (niphedipine<BR> J04813\_s\_at J04813 2114 oxidase), polypeptide 5 9.67 down 0.0107<BR> J05037\_at J05037 2116 serine dehydratase 16.24 down 0.00015<BR> J05158\_at J05158 2117 carboxypeptidase N, polypeptide 2, 83kD 8.52 down 0<BR> J05428\_at J05428 2120 UDP glycosyltransferase 2 family, polypeptide B7 16.14 down 0.00563<BR> K02100\_at K02100 2123 ornithine carbamoyltransferase 10.24 down 0.00009<BR> K02215\_at K02215 2124 angiotensinogen 16.51 down 0.00006<BR> coagulation factor IX (plasma thromboplastic<BR> K02402\_at K02402 2125 compoent, Christmas disease, hemophilia B) 28.81 down 0.00001<BR> K02766\_at K02766 2126 complement component 9 21.24 down 0<BR> cytochrome P450, subfamily IIA (phenobarbital-<BR> K03192\_f\_at K03192 2127 inducible), polypeptide 6 69.92 down 0<BR> cytochrome P450, subfamily IIA (phenobarbital-<BR> K03192\_f\_at K03192 2127 inducible), polypeptide 6 50.16 down 0<BR> L00190\_s\_at L00190 2130 antithrombin III 42.41 down 0.00012<BR> L00352\_at L00352 2131 low density lipoprotein receptor (familial 4.19 down 0.00352<BR> L00972\_at L00972 2133 cystathionine-beta-synthase 7.19 down 0.00008<BR> L04751\_at L04751 2138 cytochrome P450, subfamily IVA, polypeptide 11 36.79 down 0.00004<BR> L05144\_at L05144 2139 phosphoenolpyruvate carboxykinase 1 (soluble) 4.76 down 0.02289<BR> L05779\_at L05779 2140 epoxide hydrolase 2, cytoplasmic 5.35 down 0.00006<BR> 3-hydroxymethyl-3-methylglutaryl-Coenzyme A<BR> L07033\_at L07033 2144 lyase (hydroxymethylglutaricaciduria) 3.49 down 0<BR> enoyl-Coenzyme A, hydratase/3-hydroxyacyl<BR> L07077\_at L07077 2145 Coenzyme A dehydrogenase 4.82 down 0.00403<BR> L07765\_at L07765 2147 carboxylesterase 1 (monocyte/macrophage 20.53 down 0.00025 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank seq ID Known Gene Name Fold Change Direction Pvalue<BR> glucan (1,4-alpha-), branching enzyme 1<BR> L07956\_at L07956 2148 (glycogen branching enzyme, Andersen disease, 5.6 down 0.00029<BR> fatty-acid-Coenzyme A ligase, long-chain 1,fatty-<BR> L09229\_s\_at L09229 2150 acid-Coenzyme A ligase, long-chain 2 18.34 down 0.00016<BR> L09708\_at L09708 2152 complement component 2 3.92 down 0.00693<BR> L09717\_at L09717 2153 lysosomal-associated membrane protein 2 4.06 down 0.00034<BR> L11005\_at L11005 2154 aldehyde oxidase 1 16.3 down 0.00065<BR> L11244\_s\_at L11244 2155 complement component 4-binding protein, beta 43.33 down 0<BR> L11244\_s\_at L11244 2155 complement component 4-binding protein, beta 12.03 down 0.0001<BR> L11708\_at L11708 2158 hydroxysteroid (17-beta) dehydrogenase 2 5.99 down 0.01516<BR> L11931\_at L11931 2159 serine hydroxymethyltransferase 1 (soluble) 7.27 down 0.00041<BR> L12760\_s\_at L12760 2162 phosphoenolpyruvate carboxykinase 1 (soluble) 12.75 down 0.00035<BR> L13278\_at L13278 2163 crystallin, zeta (quinone reductase) 5.83 down 0.0034<BR> L15702\_at L15702 2165 B-factor, properdin 3.7 down 0.04693<BR> cytochrome P450, subfamily IIC (mephenytoin 4-<BR> L16883\_s\_at L16883 2166 hydroxylase), polypeptide 9 84.71 down 0.00327<BR> L17128\_at L17128 2167 gamma-glutamyl carboxylase 4.02 down 0.00096<BR> phosphodiesterase 4A, cAMP-specific (dunce<BR> L20965\_at L20965 2175 (Drosophila)-homolog phosphodiesterase E2) 3.02 down 0.01177<BR> solute carrier family 10 (sodium/bile acid<BR> L21893\_at L21893 2176 cotransporter family), member 1 13.18 down 0.00155<BR> L22548\_at L22548 2178 collagen, type XVIII, alpha 1 3.87 down 0.0299<BR> L25878\_s\_at L25878 2183 epoxide hydrolase 1, microsomal (xenobiotic) 26.84 down 0<BR> L25880\_s\_at L25880 2184 epoxide hydrolase 1, microsomal (xenobiotic) 58.7 down 0.00013<BR> L27050\_at L27050 2186 apolipoprotein F 10.26 down 0.00026<BR> L29008\_at L29008 2189 sorbitol dehydrogenase 3.51 down 0.00825<BR> L29433\_at L29433 2191 coagulation factor X 7.74 down 0.00244<BR> L32140\_at L32140 2192 afamin 17.31 down 0.00003<BR> L32179\_at



L32179 2193 arylacetamide deacetylase (esterase) 23.83 down 0<BR> bile acid Coenzyme A: amino acid N-<BR> L34081\_at L34081 2199 acyltransferase (glycine N-choloyltransferase) 11.96 down 0.00008 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> glutamate-cysteine ligase (gamma-<BR> L35546\_at L35546 2203 glutamylcysteine synthetase), regulatory (30.8kD) 14.18 down 0.00018<BR> glutamate-cysteine ligase (gamma-<BR> L35546\_at L35546 2203 glutamylcysteine synthetase), regulatory (30.8kD) 5.56 down 0.0005<BR> L36033\_at L36033 2204 stromal cell-derived factor 1 5.1 down 0.00603<BR> L38490\_s\_at L38490 2207 AdP-ribosylation factor 4-like 3.13 down 0.01306<BR> 5,10-methenyltetrahydrofolate synthetase (5-<BR> L38928\_at L38928 2209 formyltetrahydrofolate cyclo-ligase) 10.97 down 0.0267<BR> 5,10-methenyltetrahydrofolate synthetase (5-<BR> L38928\_at L38928 2209 formyltetrahydrofolate cyclo-ligase) 5.17 down 0.00726<BR> L40401\_at L40401 2211 putative protein 6.97 down 0.00079<BR> L40401\_at L40401 2211 putative protein 4.26 down 0.00194<BR> L41067\_at L41067 2213 nuclear factor of activated T-cells, cytoplasmic 3 4.96 down 0.00473<BR> L47726\_at L47726 2219 phenylalanine hydroxylase 25.63 down 0.00019<BR> L48516\_at L48516 2220 paraoxonase 3 22.21 down 0.00004<BR> L49169\_at L49169 2221 FBJ murine osteosarcoma viral oncogene 3.4 down 0.01193<BR> L76465\_at L76465 2224 hydroxyprostaglandin dehydrogenase 15-(NAD) 3.56 down 0.00688<BR> L76571\_at L76571 2226 nuclear receptor subfamily 0, group B, member 2 4.44 down 0.00312<BR> L76687\_at L76687 2227 growth factor receptor-bound protein 14 5.16 down 0.00199<BR> L76927\_rna1\_at L76927 2228 galactokinase 1 3.66 down 0.00999<BR> solute carrier family 25 (mitochondrial carrier;<BR> L77567\_s\_at L77567 2229 citrate transporter), member 1 3.14 down 0.04095<BR> M10058\_at M10058 2230 asialoglycoprotein receptor 1 23.96 down 0<BR> M10612\_at M10612 2232 apolipoprotein C-II 17.13 down 0.00746<BR> M10942\_at M10942 2233 metallothionein 1E (functional) 6.19 down 0.00428<BR> M10943\_at M10943 2234 metallothionein 1F (functional) 3.88 down 0<BR> M11025\_s\_at M11025 2235 asialoglycoprotein receptor 2 17.56 down 0.00003<BR> M11313\_s\_at M11313 2236 alpha-2-macroglobulin 10.05 down 0.00014<BR> M11321\_at M11321 2237 group-specific component (vitamin D binding 16.52 down 0.01416<BR> M11437\_cds1\_at M11437 2238 kininogen 18.38 down 0.00006<BR> M11437\_cds2\_at M11437 2238 kininogen 16.19 down 0.02277 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> M11567\_rna1\_at M11567 2239 angiogenin, ribonuclease, RNase A family, 5 32.25 down 0.0001<BR> M12174\_at M12174 2242 ras homolog gene family, member B 5.44 down 0.0088<BR> alcohol dehydrogenase 1 (class I), alpha<BR> polypeptide, alcohol dehydrogenase 2 (class I),<BR> M12272\_s\_at M12272 2243 beta polypeptide, alcohol dehydrogenase 3 (class 32.42 down 0.0034<BR> M12529\_at M12529 2244 apolipoprotein E 3.05 down 0.03776<BR> M12625\_at M12625 2245 lecithin-cholesterol acyltransferase 4.55 down 0.01584<BR> M12712\_s\_at M12712 2246 protein C (inactivator of coagulation factors Va 7.37 down 0.01866<BR> alcohol dehydrogenase 1 (class I), alpha<BR> polypeptide, alcohol dehydrogenase 2 (class I),<BR> M12963\_s\_at M12963 2248 beta polypeptide, alcohol dehydrogenase 3 (class 48.95 down 0.00104<BR> M13143\_at M13143 2249 kallikrein B plasma, (Fletcher factor) 1 10.39 down 0.00019<BR> M13149\_at M13149 2250 histidine-rich glycoprotein 18.65 down 0.02974<BR> M13232\_s\_at M13232 2251 coagulation factor VII (serum prothrombin 5.9 down 0.00014<BR> M13690\_s\_at M13690 2252 complement component 1 inhibitor (angioedema, 6.07 down 0.00045<BR> M13699\_at M13699 2253 ceruloplasmin (ferroxidase) 15.85 down 0.00012<BR> M13829\_s\_at M13829 2254 v-raf murine sarcoma 3611 viral oncogene 6.52 down 0<BR> M14058\_at M14058 2256 complement component 1, r subcomponent 6.66 down 0.00229<BR> M14091\_at M14091 2257 thyroxin-binding globulin 10.66 down 0.00024<BR> M14218\_at M14218 2259 argininosuccinate lyase 9.03 down 0.00078<BR> M14338\_at M14338 2260 protein S (alpha) 12.33 down 0<BR> phosphorylase, glycogen; liver (Hers disease,<BR> M14636\_at M14636 2262 glycogen storage disease type VI) 3.45 down 0.00133<BR> M15465\_s\_at M15465 2266 pyruvate kinase, liver and RBC 6.1 down 0.00069<BR> M15517\_cds5\_at M15517 2267 EST 22.76 down 0.03365<BR> M15656\_at M15656 2268 aldolase B, fructose-bisphosphate 96.66 down 0<BR> M16447\_at M16447 2270 quinoid

dihydropteridine reductase 6.57 down 0.00015<BR> M16474\_s\_at M16474 2271 butyrylcholinesterase  
 5.82 down 0.00113<BR> M16594\_at M16594 2272 glutathione S-transferase A2 73.21 down 0<BR>  
 M16750\_2\_at M16750 2273 pim-1 oncogene 3.08 down 0.01811<BR> M16961\_at M16961 2274  
 alpha-2-HS-glycoprotein 21.45 down 0.01175 Table 6B. Down regulated in metastatic cancers versus  
 normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction  
 Pvalue<BR> M16967\_at M16967 2275 coagulation factor V (proaccelerin, labile factor) 5.56 down  
 0.00047<BR> M16973\_at M16973 2276 complement component 8, beta polypeptide 22.75 down  
 0.00001<BR> M16974\_s\_at M16974 2277 complement component 8, alpha polypeptide 49.47 down  
 0.00046<BR> M17262\_at M17262 2278 coagulation factor II (thrombin) 44.3 down 0.00345<BR>  
 M17262\_at M17262 2278 coagulation factor II (thrombin) 14.24 down 0.00028<BR> M17466\_at  
 M17466 2279 coagulation factor XII (Haegman factor) 9.76 down 0.00285<BR> dystrophin (muscular  
 dystrophy, Duchenne and<BR> Becker types), includes DXS142, DXS164,<BR> M18533\_at M18533  
 2284 DXS206, DXS230, DXS239, DXS268, DXS269, 3.45 down 0.00313<BR> M19828\_s\_at M19828  
 2287 apolipoprotein B (including Ag(x) antigen) 29.37 down 0.00137<BR> M20218\_at M20218 2288  
 coagulation factor XI (plasma thromboplastin 6.4 down 0.00004<BR> M20786\_at M20786 2290 alpha-  
 2-plasmin inhibitor 16.95 down 0.00709<BR> M20867\_s\_at M20867 2291 glutamate dehydrogenase 1  
 17.73 down 0.00002<BR> M20902\_at M20902 2292 apolipoprotein C-I 3.14 down 0.0389<BR>  
 M21642\_at M21642 2294 antithrombin III 15.82 down 0.01027<BR> M21642\_s\_at M21642 2294  
 antithrombin III 15.23 down 0.02088<BR> M22976\_at M22976 2297 cytochrome b-5 7.39 down  
 0.02431<BR> M23161\_at M23161 2298 EST 3.44 down 0.00733<BR> M23234\_s\_at M23234 229  
 ATP-binding cassette, sub-family B (MDR/TAP), 10.05 down 0<BR> androgen receptor  
 (dihydrotestosterone receptor;<BR> testicular feminization; spinal and bulbar<BR> M23263\_at  
 M23263 2300 muscular atrophy; Kennedy disease) 4.6 down 0.00005<BR> androgen receptor  
 (dihydrotestosterone receptor;<BR> testicular feminization; spianl and bulbar<BR> M23263\_s\_at  
 M23263 2300 muscular atrophy; Kennedy disease) 3.35 down 0.02551<BR> intercellular adhesion  
 molecule 1 (CD54), human<BR> M24283\_at M24283 2303 rhinovirus receptor 3.19 down  
 0.04985<BR> M25079\_s\_at M25079 2305 hemoglobin, beta 9.15 down 0.01399<BR> M25280\_at  
 M25280 2306 selectin L (lymphocyte adhesion molecule 1) 3.39 down 0.004<BR> M26393\_s\_at  
 M26393 2309 acyl-Coenzyme A dehydrogenase, C-2 to C-3 16.27 down 0.00007<BR> M27492\_at  
 M27492 2312 interleukin 1 receptor, type I 4.62 down 0.0082 Table 6B. Down regulated in metastatic  
 cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold  
 Change Direction Pvalue<BR> M29194\_at M29194 2315 lipase, hepatic 12.18 down 0.00012<BR>  
 M29873\_s\_at M29873 2318 cytochrome P450, subfamily IIB (phenobarbital- 56.71 down 0.0054<BR>  
 M29874\_s\_at M29874 2319 cytochrome P450, subfamily IIB (phenobarbital- 18.44 down  
 0.00081<BR> M29971\_at M29971 2320 O-6-methylguanine-DNA methyltransferase 3.97 down  
 0.00424<BR> M30185\_at M30185 2321 cholesteryl ester transfer protein, plasma 3.83 down  
 0.0013<BR> M30185\_at M30185 2321 cholesteryl ester transfer protein, plasma 3.39 down  
 0.00089<BR> M30257\_s\_at M30257 2322 vascular cell adhesion molecule 1 3.11 down 0.00064<BR>  
 M30269\_at M30269 2323 nidogen (enactin) 3.4 down 0.00026<BR> M31169\_s\_at M31169 2325  
 propionyl Coenzyme A carboxylase, beta 4.65 down 0.00467<BR> M31627\_at M31627 2330 X-box  
 binding protein 1 6.97 down 0.00052<BR> cytochrome P450, subfamily I (aromatic<BR> M31667\_f\_at  
 M31667 2331 compound-inducible), polypeptide 2 4.38 down 0.00078<BR> M31994\_at M31994 2332  
 aldehyde dehydrogenase 1, soluble 11.24 down 0.01192<BR> cytochrome P450, subfamily IIA  
 (phenobarbital<BR> M33317\_f\_at M33317 2338 inducible), polypeptide 7 32.63 down 0<BR>  
 cytochrome P450, subfamily IIA (phenobarbital<BR> M3318\_r\_at M33318 2339 inducible),  
 polypeptide 6 3.21 down 0.01621<BR> M34276\_at M34276 2341 plasminogen 24.73 down  
 0.00031<BR> M35410\_s\_at M35410 2344 insulin-like growth factor binding protein 2 (36kD) 6.45  
 down 0.04517<BR> MIP-B\_at M35590 2345 small inducible cytokine A4 5.96 down 0.01225<BR>  
 MIP-B\_at M35590 2345 small inducible cytokine A4 4.74 down 0.01225<BR> MIP-B\_at M35590  
 2345 small inducible cytokine A4 4.62 down 0.01268<BR> M35878\_at M35878 2346 insulin-like  
 growth factor binding protein 3 4.3 down 0.0027<BR> glutamix-oxaloacetic transaminase 1,

soluble<BR> M37400\_at M37400 2348 (aspartate aminotransferase 1) 8.7 down 0.0004<BR> M55150\_at M55150 2352 fumarylacetoacetate 3.93 down 0.00213<BR> potassium voltage-gated channel, shaker-related<BR> M55513\_s\_at M55513 2354 subfamily, member 5 4.81 down 0.02141<BR> M55671\_at M55671 2355 protein Z, vitamin K-dependent plasma 4.74 down 0.00078<BR> M57731\_s\_at M57731 2359 GRO2 oncogene 13.87 down 0.0123<BR> M58286\_s\_at M58286 2360 tumor necrosis factor receptor superfamily, 8.15 down 0.00037 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> M58569\_s\_at M58569 2361 EST 16.15 down 0.00174<BR> M58600\_ma1\_at M58600 2362 heparin cofactor II 39.79 down 0.00034<BR> tissue factor pathway inhibitor (lipoprotein-<BR> M59499\_at M59499 2363 associated coagulation inhibitor) 5.92 down 0.0005<BR> M59815\_at M59815 2364 complement component 4A 8.02 down 0.00049<BR> sphingomyelin phosphodiesterase 1, acid<BR> M59916\_at M59916 2365 lysosomal (acid sphingomyelinase) 3.36 down 0.0038<BR> M60974\_s\_at M60974 2368 growth arrest and DNA-damage-inducible, alpha 3.48 down 0.00209<BR> cytochrome P450, subfamily IIC (mephenytoin 4-<BR> M61853\_at M61853 2369 hydroxylase), polypeptide 18 7.82 down 0.00024<BR> M61854\_s\_at M61854 2370 cytochrome P450, subfamily IIC (mephenytoin 4- 3.3 down 0.04185<BR> cytochrome P450, subfamily IIC (mephenytoin 4-<BR> M61855\_at M61855 2371 hydroxylase), polypeptide 9 38.82 down 0.00023<BR> M62403\_s\_at M62403 2373 insulin-like growth factor-binding protein 4 4.12 down 0.00226<BR> M62486\_at M62486 2374 complement component 4-binding protein, alpha 22.08 down 0.00272<BR> glutathione S-transferase M1, glutathione S-<BR> M63509\_s\_at M63509 2376 transferase M2 (muscle), glutathione S- 7.06 down 0.03887<BR> M63967\_at M63967 2378 aldehyde dehydrogenase 5 4.04 down 0.00058<BR> M64554\_ma1\_at M64554 2380 coagulation factor XIII, B polypeptide 5.87 down 0.00011<BR> glycine dehydrogenase (decarboxylating; glycine<BR> M64590\_at M64590 2381 decarboxylase, glycine cleavage system protein 6.41 down 0.00002<BR> M65131\_ma1\_at M65131 2384 methylmalonyl Coenzyme A mutase 7.44 down 0.00004<BR> M65134\_s\_at M65134 2385 complement component 5 12.01 down 0.00012<BR> M65292\_s\_at M65292 2386 H factor (complement)-like 1,H factor 1 7.56 down 0.01152<BR> M68516\_ma1\_at M68516 2387 protein C inhibitor (plasminogen activator inhibitor 20.54 down 0<BR> M68840\_at M68840 2388 monoamine oxidase A 3.96 down 0.01396<BR> M68895\_ma1\_at M68895 2390 alcohol dehydrogenase 6 (class V) 4.25 down 0.00354<BR> M69177\_at M69177 2392 monoamine oxidase B 11.64 down 0.00001<BR> M72885\_ma1\_s\_at M72885 2393 putative lymphocyte G0/G1 switch gene 6.5 down 0.03461<BR> M74587\_ma1\_s\_at M74587 2394 insulin-like growth factor binding protein 1 11.42 own 0.00274<BR> M75106\_at M75106 2397 carboxypeptidase B2 (plasma) 40.63 down 0 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> M76665\_at M76665 2398 hydroxysteroid (11-beta) dehydrogenase 1 19.22 down 0.00004<BR> M80482\_at M80482 2304 paired basic amino acid cleaving system 4 4.26 down 0.00041<BR> M81182\_s\_at M81182 2404 ATP-binding cassette, sub-family D (ALD), 3.45 down 0.00499<BR> M81349\_at M81349 2405 serum amyloid A4, constitutive 76.15 down 0.00015<BR> M83216\_s\_at M83216 2407 caldesmon 1 4.27 down 0.00037<BR> M83652\_s\_at M83652 2408 proterdin P factor, complement 6 down 0.0002<BR> M83772\_at M83772 24098 flavin containing monooxygenase 3 19.54 down 0<BR> M86826\_at M86826 2413 insulin-like growth factor binding protein, acid 3.75 down 0.01157<BR> M86873\_s\_at M86873 2414 plasminogen, plasminogen-like 17.54 down 0<BR> SWI/SNF related, matrix associated, actin<BR> M88163\_at M88163 2416 dependent regulator of chromatin, subfamily a, 3.37 down 0.00098<BR> M91432\_at M91432 2420 acyl-Coenzyme A dehydrogenase, C-4 to C-12 6.74 down 0.00008<BR> M92843\_s\_at M92843 2421 zinc finger protein homologous to Zfp-36 in 3.02 down 0.04958<BR> M93143\_at M93143 2423 plasminogen-like 10.06 down 0.00098<BR> M93405\_at M93405 2424 methylmalonate-semialdehyde dehydrogenase 23.06 down 0<BR> M94065\_s\_at M94065 2425 dihydroorotate hydrogenase 11.78 down 0.00034<BR> M94065\_at M94065 2425 dihydroorotate dehydrogenase 6.47 down 0.00013<BR> M95585\_s\_at M95585 2430 hepatic leukemia factor 4.2 down 0.00212<BR> M95767\_at M95767 2432 chitobiase, di-N-acetyl 4.94 down 0.0004<BR> glutathione S-

transferase M1, glutathione S-<BR> M96233\_s\_at M96233 2433 transferase M2 (muscle), glutathione S- 4.23 down 0.04227<BR> M96843\_at M96843 2435 EST 8.42 down 0.02394<BR> M96843\_at M96843 2435 EST 4.08 down 0.02912<BR> M99439\_at M99439 2438 transducin-like enhancer of split 4, homolog of 5.14 down 0.00001<BR> rc\_N20113\_s\_at N20113 2439 EST 5.24 down 0.01346<BR> rc\_N21079\_at N21079 2441 nucleolar cystein-rich protein 4.1 down 0.00028<BR> rc\_N21550\_at N21550 2444 EST 3.08 down 0.00006<BR> rc\_N21646\_at N21656 2446 EST 3.79 down 0.00079<BR> rc\_N22404\_at N21404 2450 EST 3.99 down 0.01152<BR> rc\_N22434\_at N21434 2451 EST 4.37 down 0.01725<BR> rc\_N22854\_s\_at N22854 2452 CASP2 and RIPK1 domain containing adaptor 3.34 down 0.0084 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_N22938\_s\_at N22938 2453 serum amyloid A4, constitutive 35.39 down 0.00128<BR> rc\_N23665\_s\_at N23665 2455 hydroxysteroid (17-beta) dehydrogenase 2 9.4 down 0.00055<BR> rc\_N23730\_s\_at N23730 2456 v-fos FBJ murine osteosarcoma viral oncogene 4.38 down 0.04395<BR> rc\_N23761\_at N23761 2457 DKFZP586G011 protein 5.41 down 0.00448<BR> N23817\_at N23817 2458 EST 3.76 down 0.00288<BR> rc\_N24879\_at N24879 2460 EST 9.44 down 0.00008<BR> rc\_N25082\_s\_at N25082 2463 amplified in osteosarcoma 5.19 down 0.00895<BR> rc\_N25193\_at N25193 2464 EST 3.13 down 0.01955<BR> protein kinase, cAMP-dependent, regulatory, type<BR> rc\_N25969\_s\_at N25969 2466 I, alpha (tissue specific extinguisher 1) 4.32 down 0.00304<BR> rc\_N26184\_at N26184 2467 MYLE protein 4.82 down 0.00056<BR> rc\_N27524\_at N27524 2472 EST 3.13 down 0.00216<BR> rc\_N27563\_at N27563 2473 EST 3.3 down 0.00021<BR> N27670\_at N27670 2474 progesterone membrane binding protein 6.15 down 0.00321<BR> rc\_N27834\_at N27834 2475 alpha2,3-sialyltransferase 5.31 down 0.00039<BR> rc\_N29319\_at N29319 2476 EST 4.58 down 0.00011<BR> rc\_N29353\_at N29353 2477 kynurenine 3-monooxygenase (kynurenine 3- 4.78 down 0.00019<BR> rc\_N30856\_at N30856 2485 solute carrier family 19 (thiamine transporter), 3.71 down 0.00393<BR> rc\_N31598\_at N31598 2488 EST 3.1 down 0.00203<BR> rc\_N31741\_at N31741 2489 serien hydroxymethyltransferase 1 (soluble) 14.76 down 0.00001<BR> rc\_N31952\_at N31952 2490 est 3.13 down 0.01481<BR> rc\_N32071\_at N32071 2491 est 8.75 down 0.00006<BR> rc\_N33009\_s\_at N33009 2492 apolipoprotein E 60.54 down 0.0093<BR> rc\_N34441\_at N34441 2496 EST 3.07 down 0.00186<BR> rc\_N34804\_at N34804 2497 DKFZP434J214 protein 8.08 down 0.00028<BR> rc\_N36001\_at N36001 2504 EST 6.16 down 0.00222<BR> rc\_N36250\_at N36250 2506 cellular repressor of E1A-stimulated genes 4.06 down 0.00776<BR> rc\_N39163\_at N39163 2509 metallothionein 1L 4.3 down 0.03917<BR> rc\_N39201\_at N39201 2510 protease inhibitor 4 (kallistatin) 24.91 down 0.000253<BR> rc\_N40188\_at N40188 2513 EST 3.72 down 0.01771<BR> N40320\_at N40320 2514 est 7.56 DOWN 0.01584 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_N45232\_at N45232 2517 EST 3.61 down 0.01308<BR> rc\_N45307\_s\_at N45307 2518 EST 4.55 down 0.00006<BR> rc\_N45998\_at N45998 2520 EST 3.14 down 0.00337<BR> rc\_N474689\_at N47469 2522 EST 3.34 down 0.00329<BR> rc\_N47942\_at N47942 2523 progesterone membrane binding protein 4.51 down 0.00168<BR> rc\_N48180\_at N48180 2526 EST 3.36 down 0.00543<BR> rc\_N48315\_at N48315 2527 adaptor-related protein complex 2, mu 2 subunit 5.3 down 0.0149<BR> rc\_N48602\_at N48602 2529 EST 3.17 down 0.02913<BR> rc\_N48674\_at N48674 2530 EST 4.06 down 0.00028<BR> rc\_N48787\_at N48787 2531 protease inhibitor 1 (anti-elastase), alpha-1- 4.4 down 0.00292<BR> rc\_N49090\_at N49090 2533 EST 18 down 0.00501<BR> rc\_N49104\_s\_at N49104 2534 nuclear receptor interacting protein 1 3.83 down 0.00144<BR> rc\_N49113\_at N49113 2535 EST 3.4 down 0.00162<BR> rc\_N49214\_at N49214 2536 EST 4.74 down 0.00064<BR> rc\_N49595\_at N49595 2538 EST 10.39 down 0.00022<BR> rc\_N49902\_at N49902 2540 EST 3.55 down 0.00455<BR> rc\_N51117\_at N51117 2544 EST 9.68 down 0.00081<BR> rc\_N51737\_at N51737 2547 mitogen-activated protein kinase kinase kinase 3.32 down 0.00376<BR> rc\_N51773\_at N51773 2549 EST 16.32 down 0.0007<BR> rc\_N52271\_at N52271 2552 LIM protein (similar to rat protein kinase C- 8.06 down 0.00011<BR> rc\_N52322\_at N52322 2553 EST 3.27 down 0.00933<BR> rc\_N52845\_at N52845 2554 EST 5.53 down 0.00088<BR> rc\_N52985\_at N52985 2555

nidogen (enactin) 4.21 down 0.01385<BR> rc\_N53031\_s\_at N53031 2556 UDP glycosyltransferase 2 family, polypeptide B4 97.58 down 0.00022<BR> rc\_N53352\_at N53352 2558 EST 3.22 down 0.00416<BR> cytochrome P450 subfamily III (arachidonic acid<BR> rc\_N53549\_s\_at N53549 2559 epoxygenase) polypeptide 2 4.68 down 0.00818<BR> rc\_N53757\_at N53757 2560 EST 3.97 down 0.00255<BR> rc\_N54053\_at N54053 2561 secreted phosphoprotein 2, 24D 60.39 down 0.00087<BR> rc\_N54311\_at N54311 2564 EST 4.82 down 0.00183<BR> rc\_N54399\_at N54399 2566 EST 3.34 down 0.00048 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_N54417\_s\_at N54417 2567 fibrinogen, A alpha polypeptide 99.28 down 0.00001<BR> rc\_N54429\_at N54429 2568 EST4 57.81 down 0.00724<BR> rc\_N54511\_s\_at N54511 2569 KIAA0265 protein 3.45 down 0.03362<BR> rc\_N54604\_at N54604 2570 EST 3.72 down 0.00741<BR> cytidine monophosphate-N-acetylneuraminic acid<BR> rc\_N54792\_at n54792 2571 hydroxylase (CMP-N-acetylneuroamate 3.23 down 0.00099<BR> rc\_N54950\_s\_at N54950 2573 ketohexokinase (fructokinase) 17.17 down 0.00078<BR> N57464\_at N57464 2576 CCAAT/enhancer binding protein (C/EBP), delta 14.69 down 0.00018<BR> rc\_N57934\_s\_at N57934 2577 formininotrasferase cyclodeaminase 13.81 down 0.00171<BR> rc\_N58326\_at N58326 2579 EST 14.97 down 0.00647<BR> rc\_N59089\_at N59089 2581 EST 4.74 down 0.00055<BR> rc\_N59231\_s\_at N59231 2582 pyruvate carboxylase 3.45 down 0.2066<BR> rc\_N59283\_at N5283 2583 EST 4.65 down 0.02343<BR> rc\_N59474\_at N59474 2584 EST 6.93 down 0.00337<BR> rc\_N59532\_s\_at N59532 2585 ainomethyltransferase (glycine cleavage 6.73 down 0.00005<BR> rc\_N59543\_at N59543 2587 PDZ domaine containing 1 9.96 down 0.00052<BR> rc\_N59550\_at N59550 2588 EST 25.56 down 0.00024<BR> rc\_N62443\_at N62443 2590 EST3.72 down 0.01717<BR> rc\_N62523\_at N62523 2592 hepatic leukemia factor 5.02 down 0.00087<BR> rc\_N62652\_s\_at N62652 2593 EST 5.23 down 0.03006<BR> rc\_N63391\_at N63391 2600 EST 7.39 down 0.00565<BR> rc\_N63688\_at n^3688 2603 EST 3.13 down 0.002<BR> rc\_N63698\_at N63698 2604 EST 7.92 down 0.00001<BR> rc\_N63845\_at N63845 2605 phytanoyl-CoA dhydroxylase (Refsum disease) 25.92 down 0.00084<BR> rc\_N64017\_at N64017 2606 EST 5.27 down 0.00022<BR> enoyl-Coenzyme A, hydratase/3-hydroxyacyl<BR> rc\_N64036\_s\_at N64036 2607 Coenzyme A dehydrogenase 9.99 down 0.00125<BR> rc\_N64436\_at N64436 2609 EST 3.51 down 0.00441<BR> rc\_N64535\_at N64535 2610 EST 6.19 down 0.00106<BR> rc\_N65959\_at4 N65959 2612 EST 5.43 down 0.00044<BR> rc\_N66066\_at N66066 2613 EST 28.35 down 0.00055 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction pvalue<BR> rc\_N66130\_at N66130 2614 progesterone membrane binding protein 3.98 down 0.0106<BR> rc\_N66422\_at N66422 2616 EST 4.1 down 0.00237<BR> rc\_N66763\_at N66763 2619 EST 3.79 down 0.03015<BR> rc\_N66857\_at4 N66857 2620 EST 15.03 down 0.00005<BR> prion protein (p27-30) (Creutzfeld-Jakob disease,<BR> rc\_N67009\_s\_at N67009 2622 Gerstmann Strausler-Scheinker syndrome, fatal 3.55 down 0.00956<BR> rc\_N67096\_at N67096 2623 EST 3.23 down 0.00446<BR> rc\_N67105\_at N67105 2624 EST 5.01 down 0.00176<BR> rc\_N67378\_at N67378 2626 KIAA1053 protein 7.14 down 0<BR> re\_N67876\_s\_at N67876 2628e insulin-like growth factor 1 (somatomedin C) 8.89 down 0.00042<BR> rc\_N67893i\_at N67893 2629 EST 10.48 down 0.00341<BR> rc\_N68596\_s\_at4 N68596 2636 betain-homocysteine methyltransferase 40.99 down 0<BR> rc\_N68730\_at N68730 2637 EST 3.88 down 0.00091<BR> rc\_N68974\_at N68974 2640 EST 16.44 down 0.00087<BR> rc\_N68993\_at n68993 2641 EST 3.06 down 0.00867<BR> rc\_N69136\_at N69136 2645 EST 18.53 down 0.00366<BR> rc\_N69216\_at N69216 2646 EST 3.4 down 0.00497<BR> rc\_N69299\_at N69299 2649 EST 3.63 down 0.03776<BR> rc\_N70005\_at N70005 2653 EST 3.42 down 0.04229<BR> rc\_N70057\_s\_at4 N70057 2654 DNA segment on chromosome 6 (unique) 49 5.24 down 0.01178<BR> rc\_N70305\_at N70305 2655 EST 4.41 down 0.00078<BR> rc\_N70358\_s\_at N70358 2657 growth hormone receptor 34.35 down 0<BR> rc\_N70861\_at N70861 2661 EST 6.55 down 0.00001<BR> solute carrier faily 10 9sodium/bile acid<BR> rc\_N70966\_s\_at N70966 2663 co4transporter family), member 1 34.06 down 0.0006<BR> rc\_N71542-at N71542 2665 kidney-and live-specific gene 21.05 down0<BR> rc\_n71935\_s\_at N71935 2667 multiple PDZ domain protein 16.28 down 0<BR> rc\_N72259\_at N72259



2670 cornichon-lie 4.65 down 0.0054<BR> rc\_N76295\_s\_at N72695 2671 EST 9.18 down 0.00069<BR> rc\_N73461\_f\_at N73461 2673 EST 4.25 down 0.00162<BR> rc\_N73468\_s\_at N73468 2674 protein S (alpha) 4.4 down 0.00853 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_N73543-at N73543 2675 EST 17 down 0.00003<BR> rc\_N73561\_at4 N73561 2676 Est 12.96 down 0.00011<BR> rc\_N73883i\_at N73883i 2682 EST 9.35 down 0<BR> rc-N73998\_at N73988 2683 EST 10.27 down 0.00083<BR> rc\_N74025\_at N74025 2685 deiodinase, iodothyronine, type I 22.79 down 0<BR> rc\_N74422-at N74422 2686 EST 30.32 down 0<BR> rc\_N74558\_at N74558 2687 EST 3.19 down 0.00247<BR> rc\_N75072\_at4 N75072 2689 EST 3.73 down 0.00379<BR> n75203\_s\_at N75203 2691 EST 6.15 down 0.00181<BR> N75870\_s\_at N75870 2693 dual specificity phosphatase 1 13.41 down 0.00251<BR> rc\_N76012\_r-at N76012 e2694 EST 36.71 down 0.00598<BR> N77326\_at N77326 2696 EST 7.51 down 0.00542<BR> N77606\_at N77606 2697 EST 4.22 down 0.00119<BR> macrophage stimulating 1 (hepatocyte growth<BR> rc\_N788i50\_s\_at N78850 2699 factor-like), macrophage stimulation, pseudogene 13.69 down 0.00421<BR> rc\_N78902i\_at N789022 2700 leptin receptor 6.79 down 0.0041<BR> rc\_N79435-at N79435 2701 chromosome 15 open reading frame 3 3.73 down 0.00861<BR> rc\_N79778\_at N79778 2702 extracellular matrix protein 2, female organ and 5.15 down 0.00286<BR> rc\_N80129\_i\_at N80129 2703 metallothionein 1L 66.48 down 0.00415<BR> rc\_N810129\_f\_at N80129 2703 metallothionein 1L 13.6 down 0.00196<BR> rc\_N81025\_at N81025 2705 EST 8.61 down 0.00015<BR> rc\_n81036\_at4 N81036 2706 EST 6.89 down 0.00276<BR> N89302\_s\_at N89302 2708 HLA-B associated transcript-3 23.44 down 0.00192<BR> rc\_N89738\_at N89738 2710 Est 10.06 down 0.00052<BR> rc\_N90584\_at N90584 2714 EST 3.08 down 0.02602<BR> N90820\_at N90820 2715 DKFZP566B1346 protein 4.86 down 0.03008<BR> N91087\_at N91087 2717 EST 6.91 down 0.00109<BR> rc\_N91273\_r\_at N91273 2718 EST 4.07 down 0.02965<BR> rc\_N91882\_at N91882 2720 alpha2,3-sialyltransferase 14.52 down 0.00024<BR> rc\_N93155\_f\_at N93155 2729 clamodulin 1 (Phosphorylase kinase, delta) 4.39 down 0.0002<BR> rc\_N93155\_i\_at N93155 2729 calmodulin 1 (Phosphorylase kinase, delta) 3.46 down 0.00031 Table 6B. Down regulated in metastatic cancers versus normal sample set2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction pvalue<BR> IC\_N93i191\_at4 N93191 2730 EST 3.25 down 0.00232<BR> rc\_N93246\_f\_at N93246 2731 EST 3.03 down 0.00049<BR> rc\_N93764\_at N93764 2737 EST 5.92 down 0.0109<BR> n94146\_at N94146 2739 EST 8.05 down 0<BR> rc\_N94367\_at N94367 2740 est 8.79 down 0.01003<BR> rc\_N94930\_at N94930 2741 multiple PDZ domain protein 10.06 down 0.00226<BR> rc\_N95495\_at N95495 2742 EST 5.61 down 0.00308<BR> rc\_N95585\_at N95585 2743 EST 3.1 down 0.0083<BR> N99542\_at N99542 2747 orosomucoid 1 8.41 down 0.00001<BR> rc\_N99866\_at N99866 2748 EST 3.13 down 0.04148<BR> rc\_R00296\_at R00296 2750 EST 3.98 down 0.04632<BR> rc\_R00843\_s\_at R00843 2741 fragile histidine triad gene 3.68 down 0.03578<BR> rc\_R01023\_s\_at R01023 2752 glucokinase (hexokinase 4) regulatory protein 50.71 down 0.00321<BR> rc\_R01081\_at R01081 2753 EST 3.3 down 0.00839<BR> glucose-6-phosphatase, catalytic (glycogen<BR> rc\_R02365\_f\_at R02365 2755 storage disease type 1, von Gierke disease) 17.17 down 0.00124<BR> rc\_R02371\_at R02371 2756 EST 3.57 down 0.00009<BR> rc\_R02572\_at R02572 2757 fibronectin 1 7.1 down 0.00059<BR> rc\_R02752\_at R02752 2758 EST 3.05 down 0.00362<BR> rc\_R05309\_f\_at R05309 2759 EST 3.72 down 0.0008<BR> rc\_R05490\_at R05490 2761 SEC24 (S. cerevisiae) related gene family, 3.03 down 0.00317<BR> rc\_R05518\_at R05518 2762 EST 4.15 down 0.0125<BR> rc\_R06002\_s\_at R06002 2763 EST 10.15 down 0.00003<BR> rc\_R06271\_s\_at R06271 2766 EST 6.14 down 0.000063<BR> rc\_R06726\_s\_at R06726 2770 aprotease inhibitor 1 (anti-elastase), alpha-1 12.26 down 0.03905<BR> rc\_R06746\_at R06746 2771 EST 15.77 down 0.00009<BR> rc\_R06764\_s\_at R06764 2772 apolipoprotein Ag(x) antigen) 4.91 down 0.00167<BR> rc\_R06977\_f\_at R06977 2775 glucokinase (hexokinase 4) regulatory protein 6.1 down 0.00049<BR> rc\_R07637-at R07637 2778 EST 3.04 down 0.00118<BR> rc\_R08548\_at R08548 2779 EST 9.94 down 0.00326<BR> rc\_R08564\_at R08564 2780 plasminogen-like 60.18 down 0.00091 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR>



rc\_R08615\_s\_at R08615 2781 homogentisate 1,2-dioxygenase (homogentisate 21.85 down 0.00026<BR> rc\_R09053\_at R08850 2782 EST 12.55 down 0.00009<BR> rc\_R09053\_at R09053 2783 EST 5.9 down 0.0002<BR> rc\_R10138\_at R10138 2784 EST 4 down 0.00032<BR> rc\_R10287\_at R10287 2785 EST 11.2 down 0.0003<BR> rc\_R10378\_s\_at R10378 2786 fibrinogen-like 1 8.13 down 0.00189<BR> rc\_R10662\_f\_at R10662 2787 mutL (E. coli) homolog 1 (colon cancer, 3.2 down 0.0005<BR> rc\_R10684\_at R10684 2788 EST 5.51 down 0.00741<BR> rc\_R12472\_at R12742 2789 EST 55.18 down 0.00011<BR> rc\_R12579\_at R12579 2790 EST 3.5 down 0.00137<BR> rc\_R15825\_r\_at R15825 2792 KIAA0946 protein; Huntingtin interacting protein 5.33 down 0.00391<BR> rc\_R16098\_at R16098 2793 EST 63.41 down 0.00038<BR> rc\_R17762\_at R17762 2795 EST 3.37 down 0.01822<BR> rc\_R21232\_at R21232 2798 EST 3.56 down 0.00246<BR> rc\_R22196\_at R22196 2799 EST 3.75 down 0.02867<BR> rc\_R22905\_at R22905 2801 EST 4.64 down 0.0043<BR> rc\_R26904\_f\_at R26904 2805 EST 3.51 down 0.00058<BR> R31641\_at R31641 2814 EST 9.96 down 0.00011<BR> rc\_R31917\_s\_at R31917 2815 EST 3.91 down 0.00071<BR> rc\_R32036\_s\_at R32036 2816 interleukin 1 receptor-like 1 4.02 down 0.00051<BR> rc\_R32440\_at R32440 2817 EST 7.41 down 0.00159<BR> rc\_R32490\_s\_at R32490 2818 EST 8.95 down 0.00215<BR> rc\_R33146\_at R33146 2819 EST 7 down 0.00043<BR> rc\_R34133\_at R34133 2821 EST 4.13 down 0.00008<BR> rc\_R34362\_at R34362 2822 KIAA0327 gene product 5.4 down 0.04615<BR> rc\_R36228\_at R36228 2824 EST 4.39 down 0.00033<BR> rc\_R36989\_s\_at R36989 2826 hypothetical protein, estradiol-induced 13.7 down 0.00056<BR> rc\_R37128\_s\_at R37128 2827 complement component 4A 39.51 down 0.00364<BR> rc\_R38185\_at R38185 2829 EST 6.32 down 0.00063<BR> rc\_R38709\_s\_at R38709 2833 superoxide dismutase 2, mitochondrial 8.23 down 0.01578<BR> rc\_R39234\_r\_at R39234 2835 EST 3.24 down 0.0412 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq iD Known Gene Name Fold Change Direction Pvalue<BR> rc\_R40395\_s\_at R40395 2841 lecithin-cholesterol acyltransferase 37.33 down 0.00032<BR> rc\_R40492\_at R40492 2842 EST 8.89 down 0.00229<BR> rc\_R40556\_s\_at R40556 2843 EST 3.57 down 0.00184<BR> rc\_R40899\_f\_at R40899 2844 glycine receptor, beta 9.11 down 0.0009<BR> rc\_R40946\_f\_at R40946 2845 crystallin, zeta (quinone reductase) 6.14 down 0.00156<BR> rc\_R42241\_at R42241 2846 EST 3.97 down 0.00129<BR> rc\_R43166\_i\_at R43166 2847 EST 3.37 down 0.00919<BR> rc\_R43174\_s\_at R43174 2848 paraoxonase 1 74.04 down 0.00038<BR> rc\_R43365\_at R43365 2850 EST 5.37 down 0.00103<BR> rc\_R43799\_at R43799 2851 EST 16.35 down 0.00208<BR> rc\_R43910\_at R43910 2852 EST 5.71 down 0<BR> rc\_R44025\_at R44025 2854 EST 4.4 down 0.01325<BR> rc\_R44761\_at R44761 2858 aryl hydrocarbon receptor nuclear translocator 3.12 down 0.02663<BR> rc\_R45656\_i\_at R45656 2865 EST 10.21 down 0.00179<BR> rc\_R48307\_at R48307 2870 EST 7.18 down 0.00007<BR> rc\_R48540\_s\_at R48540 2873 EST 6.05 down 0.00086<BR> rc\_R48732\_s\_at R48732 2876 EST 5.12 down 0.00837<BR> rc\_R49035\_at R49035 2877 EST 8.02 down 0.00991<BR> rc\_R49459\_s\_at R49459 2882 transferrin receptor 2 85.61 down 0.00048<BR> rc\_R49602\_at R49602 2885 EST 36.5 down 0.00001<BR> R50008\_s\_at R50008 2887 7-dehydrocholesterol reductase 6.67 down 0.00409<BR> rc\_R51256\_at R51256 2889 EST 3.04 down 0.00286<BR> rc\_R51309\_at R51309 2890 KIAA1077 protein 3.54 down 0.04112<BR> rc\_R51831\_at R51831 2891 EST 5.03 down 0.00761<BR> rc\_R52800\_at R52800 2895 EST 3.96 down 0.00749<BR> rc\_R52822\_i\_at R52822 2896 EST 12.79 down 0.00001<BR> rc\_R52949\_at R52949 2897 EST 3.46 down 0.00395<BR> rc\_R54416\_at R54416 2901 EST 3.14 down 0.00236<BR> rc\_R56094\_at R56094 2905 EST 4.87 down 0.00214<BR> rc\_R56602\_at R56602 2907 Ig superfamily protein 3.06 down 0.02464<BR> rc\_R59221-at R59221 2912 progesterone binding protein 7.54 down 0.00159 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_R59325\_at R59325 2914 EST 4.48 down 0.00117<BR> rc\_R59722\_at R59722 2916 EST 19.74 down 0.00016<BR> rc\_R61740\_f\_at R61740 2923 EST 4.02 down 0.00321<BR> rc\_R62173\_f\_at R62173 2924 UDP-glucose dehydrogenase 5.76 down 0.0006<BR> rc\_R62519\_f\_at R62519 2926 EST 10.83 down 0.00243<BR> R63545\_at R63545 2927 EST 5.4 down 0.00202<BR> rc\_R64131\_at R64131 2930 EST 20.58 down 0.01028<BR> rc\_R64144\_s\_at R64144 2932 cAMP responsive element

binding protein-like 2 4.58 down 0.00495<BR> R64199\_at R64199 2933 SEC22, vesicle trafficking protein (S. cerevisiae)- 9.19 down 0.00387<BR> rc\_R65593\_s\_at R65593 2935 kynurenine 3-monooxygenase (kynurenine 3- 21.27 down 0.00007<BR> R67751\_at R67751 2939 EST 3.12 down 0.00319<BR> rc\_R67970\_s\_at R67970 2940 gamma-glutamyl carboxylase 9.45 down 0.00212<BR> rc\_R69031\_at R69031 2941 EST 3.19 down 0.00798<BR> R69417\_at R69417 2942 EST 7.79 down 0.03795<BR> rc\_R70790\_at R70790 2948 EST 4.07 down 0.02354<BR> rc\_R71491\_at R71491 2954 EST 3.55 down 0.01903<BR> rc\_R73485\_at R73485 2958 EST 7.77 down 0.0009<BR> rc\_R73816\_at R73816 2961 EST 11.53 down 0.00259<BR> R77628\_at R77628 2966 insulin induced gene 1 29.23 down 0.00122<BR> R80048\_at R80048 2972 EST 12.28 down 0.00128<BR> R80573\_at R80573 2973 EST 3.08 down 0.02126<BR> rc\_R82074\_f\_at R82074 2974 syndecan 1 6.66 down 0.01336<BR> R82229\_at R82229 2975 phosphatidylserine decarboxylase 3.08 down 0.03455<BR> rc\_R82837\_at R82837 2976 KIAA0970 protein 5 down 0.00181<BR> R87373\_s\_at R87373 2978 EST 4.09 down 0.02253<BR> rc\_R89811\_s\_at R89811 2980 HGF activator 62.51 down 0.00148<BR> rc\_R91503\_s\_at R91503 2982 ATP\_binding cassette, sub-family C (CFTR/MRP), 9.64 down 0.00584<BR> rc\_R92458\_f\_at R92458 2986 hemoglobin, gamma G 3.31 down 0.00763<BR> rc\_R92475\_s\_at R92475 2987 flavin containing monooxygenase 3 26.13 down 0<BR> rc\_R92737\_at R92737 2988 EST 4.53 down 0.04447<BR> rc\_R92768\_at R92768 2989 EST 13.2 down 0.00001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_R93714\_at R93714 2992 fetuin B 10.42 down 0.00043<BR> R93776\_s\_at R93776 2993 EST 39.32 down 0.00176<BR> rc\_R93908\_at R93908 2994 EST 5.8 down 0.02699<BR> R94662\_at R94662 2995 heme-binding protein 4.41 down 0.02301<BR> rc\_R94674\_s\_at R94674 2996 EST 10.76 down 0.00008<BR> R96417\_at R96417 2998 EST 3.9 down 0.00019<BR> rc\_R96822\_at R96822 3000 EST 8.25 down 0.00008<BR> rc\_R97302\_at R97302 3003 EST 3.73 down 0.01887<BR> cytochrome P450, subfamily VIIIB (sterol 12<BR> rc\_R97419\_at R97419 3004 alpha hydroxylase), polypeptide 1 65.07 down 0.0039<BR> rc\_R97711\_at R97711 3005 EST 3.37 down 0.00838<BR> rc\_R97798\_at R97798 3007 EST 3.79 down 0.00015<BR> R98073\_at R98073 3009 EST 46.87 down 0<BR> rc\_R98074\_at R98074 3010 EST 9.21 down 0.00048<BR> rc\_R98413\_at R98413 3012 EST 9.71 down 0.00007<BR> rc\_R98624\_at R98624 3013 EST 21.32 down 0<BR> rc\_R98774\_at R98774 3014 EST 3.93 down 0.00001<BR> rc\_R99591\_at R99591 3016 CD5 antigen-like (scavenger receptor cysteine 9.52 down 0.00006<BR> rc\_R99909\_at R99909 3017 EST 4.27 down 0.00045<BR> S48983\_at S48983 3018 serum amyloid A4, constitutive 23.04 down 0.00022<BR> S52028\_s\_at S52028 3019 cystathionase (cystathionine gamma-lyase) 3.21 down 0.00476<BR> S62539\_s\_at S62539 3022 insulin receptor substrate 1 3.7 down 0.01307<BR> S67325\_at S67325 3024 propionyl Coenzyme A carboxylase, beta 4.19 down 0.00151<BR> aldo-keto reductase family 1, member C4<BR> (chlordecone reductase; 3-alpha hydroxysteroid<BR> S68287\_at S68287 3025 dehydrogenase, type I; dihydrodiol 24.11 down 0<BR> S68805\_at S68805 3026 glycine amidinotransferase (L-arginine:glycine 18.19 down 0.00083<BR> S69232\_at S69232 3027 electron-transferring-flavoprotein dehydrogenase 4.9 down 0.00017<BR> S70004\_at S70004 3029 glycogen synthase 2 (liver) 9.96 down 0.00001<BR> S72370\_at S72370 3030 pyruvate carboxylase 5.31 down 0.00075<BR> S72370\_at S72370 3030 pyruvate carboxylase 4.54 down 0.0001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> S74728\_at S74728 3033 antiquitin 1 5.01 down 0.00008<BR> S77356\_at S77356 3034 EST 5.83 down 0.00122<BR> S77410\_at S77410 3035 angiotensin receptor 1 10.4 down 0<BR> S90469\_at S90469 3040 P450 (cytochrome) oxidoreductase 4.32 down 0.0182<BR> S95936\_at S95936 3041 transferrin 19.76 down 0.02009<BR> rc\_T03441\_f\_at T03441 3044 cytochrome b-561 5.74 down 0.02781<BR> rc\_T03651\_s\_at T03651 3047 tubulin, beta polypeptide 6.47 down 0.00843<BR> T08879\_at T08879 3049 cathepsin F 5.29 down 0.0008<BR> rc\_T10108\_s\_at T10108 3050 EST 3.85 down 0.01155<BR> rc\_t10264\_s\_at T10264 3051 EST 3.84 down 0.00874<BR> rc\_T10322\_at T10322 3053 dihydropyrimidinase-like 2 4.23 down 0.01527<BR> rc\_T10822\_at T10822 3055 EST 3.16 down 0.00635<BR> rc\_T15482\_f\_at T15482 3060 EST 5.04 down 0.00233<BR> rc\_T15674\_f\_at T15674 3061 EST 4.12 down 0.02111<BR> rc\_T16175\_s\_at

T16175 3064 protein tyrosine phosphatase, non-receptor type 3.07 down 0.01007<BR> rc\_T16269\_at  
 T16269 3067 EST 3.36 down 0.00282<BR> rc\_T16478\_at T16478 3070 EST 4 down 0.01041<BR>  
 rc\_T16484\_s\_at T16484 3071 EST 7.69 down 0.00805<BR> rc\_T17411\_s\_at T17411 3078  
 transthyretin (prealbumin, amyloidosis type I) 13.49 down 0.00203<BR> rc\_T23430\_at T23430 3080  
 EST 3.12 down 0.00949<BR> rc\_T23680\_at T23680 3084 calcium channel, voltage-dependent,  
 gamma 3.29 down 0.0003<BR> rc\_T23882\_s\_at T23882 3085 kininogen 42.85 down 0.00641<BR>  
 rc\_T23986\_s\_at T23986 3086 hydroxyacyl glutathione hydrolase; glyoxylase 2 7.26 down 0.0062<BR>  
 rc\_T24055\_s\_at T24055 3087 ribosomal protein L26 3.9 down 0.00046<BR> rc\_T24106\_at T24106  
 3089 EST 12.13 down 0.01687<BR> rc\_T25506\_at T25506 3090 EST 4.51 down 0.00529<BR>  
 T30341\_s\_at T30341 3101 EST 3.04 down 0.04567<BR> rc\_T33011\_at T33011 3104 EST 3.57 down  
 0.02486<BR> T39897\_s\_at T39897 3114 androgen induced protein 10 down 0.00466<BR>  
 rc\_T40936\_at T40936 3118 EST 46.92 down 0.00056<BR> rc\_T40995\_f\_at T40995 3119 alcohol  
 dehydrogenase 3 (class I), gamma 13.25 down 0.01531 Table 6B. Down regulated in metastatic cancers  
 versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change  
 Direction Pvalue<BR> rc\_T41047\_s\_at T41047 3120 EST 4.74 down 0.00015<BR> rc\_T41232\_at  
 T41232 3122 EST 3.57 down 0.00846<BR> rc\_T46901\_at T46901 3123 EST 77.28 down 0.0006<BR>  
 rc\_T47778\_s\_at T47778 3127 fibrinogen, A alpha polypeptide 30 down 0.01401<BR> rc\_T48039\_s\_at  
 T48039 3129 protein C (inactivator of coagulation factor Va 84.39 down 0.00112<BR>  
 rc\_T48075\_f\_at T48075 3130 hemoglobin, alpha 1 32.56 down 0.00172<BR> rc\_T48278\_at T48278  
 3132 EST 15.02 down 0.04751<BR> rc\_T48980\_s\_at T48980 3134 calmodulin 1 (phosphorylase  
 kinase, delta) 4.2 down 0.0046<BR> rc\_T49061\_at T49061 3135 EST 3.06 down 0.00768<BR>  
 rc\_T51150\_at T51150 3137 EST 10.52 down 0.00377<BR> solute carrier family 22  
 (extraneuronal<BR> rc\_T51617\_at T51617 3138 monoamine transporter), member 3 17.67 down  
 0.00018<BR> rc\_T51930\_at T51930 3139 EST 9.99 down 0.00066<BR> rc\_T52564\_at T52564 3141  
 EST 3.28 down 0.01506<BR> rc\_T52813\_s\_at T52813 3142 putative lymphocyte G0/G1 switch gene  
 16.71 down 0.03897<BR> rc\_T54160\_s\_at T54160 3145 EST 3.24 down 0.00168<BR> rc\_T55547\_at  
 T55547 3148 EST 3.28 down 0.00047<BR> rc\_T56264\_s\_at T56264 3149 apolipoprotein C-II 53.04  
 down 0.00938<BR> rc\_T56278\_s\_at T56278 3150 H factor (complement)-like 3 28.39 down  
 0.00016<BR> rc\_T56281\_f\_at T56281 3151 RNA helicase-related protein 32.34 down 0.00002<BR>  
 T57140\_s\_at T57140 3152 paraoxonase 3 28.8 down 0<BR> rc\_T58032\_s\_at T58032 3153 3-  
 hydroxyanthranilate 3,4-dioxygenase 8.86 down 0.00023<BR> rc\_T58756\_at T58756 3156 EST 13.39  
 down 0.00013<BR> rc\_T58775\_at T58775 3157 small inducible cytokine subfamily A (Cys-Cys),  
 21.18 down 0.00006<BR> rc\_T59148\_s\_at T59148 3158 carbamoyl-phosphate synthetase 1,  
 mitochondrial 88.889 down 0<BR> rc\_T60407\_at T60407 3161 EST 6.6 down 0.00167<BR>  
 rc\_T61256\_s\_at T61256 3162 ketohexokinase (fructokinase) 13.59 down 0.00425<BR> vitronectin  
 (serum spreading factor, somatomedin<BR> rc\_T61373\_s\_at T61373 3163 B, complement S-protein)  
 44.9 down 0.03172<BR> rc\_T61389\_f\_at T61389 3164 haptoglobin 18.95 down 0.04873<BR>  
 rc\_T61649\_f\_at T61649 3165 superoxide dismutase 2, mitochondrial 26.09 down 0.00734 Table 6B.  
 Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID  
 Known Gene Name Fold Change Direction Pvalue<BR> rc\_T61801\_s\_at T61801 3167 hemopexin 25.7  
 down 0.01362<BR> rc\_T63364\_at T63364 3170 ficolin (collagen/fibrinogen domain-containing) 3 6.72  
 down 0.00383<BR> rc\_T63490\_at T63490 3171 EST 16.54 down 0<BR> rc\_T64575\_s\_at T64575  
 3172 EST 10.46 down 0.00014<BR> rc\_T64887\_f\_at T64887 3173 protein phosphatase 5, catalytic  
 subunit 5.66 down 0.00349<BR> rc\_T65972\_at T65972 3177 EST 3.21 down 0.04847<BR>  
 rc\_T66189\_s\_at T66189 3178 glutaryl-Coenzyme A dehydrogenase 8.61 down 0.00003<BR> succinate  
 dehydrogenase complex, subunit D,<BR> T67231\_at T67231 3181 integral membrane protein 7.04  
 down 0.03554<BR> rc\_T67705\_s\_at T67705 3183 asialoglycoprotein receptor 2 31.6 down  
 0.00705<BR> rc\_T67931\_at T67931 3184 fibrinogen, B beta polypeptide 49.55 down 0<BR>  
 T68083\_at T68083 3185 short-chain dehydrogenase/reductase 1 4.03 down 0.01593<BR>  
 rc\_T68426\_s\_at T68426 3186 CD81 antigen (target of antiproliferative antibody 3.11 down  
 0.01634<BR> T68510\_at T68510 3187 EST 3.87 down 0.00617<BR> rc\_T68711\_at T68711 3188 EST

37.65 down 0.00036<BR> rc\_T68855\_at T68855 3189 EST 34.04 down 0<BR> rc\_T68873\_f\_at T68873 3190 metallothionein 1L 28.72 down 0.02953<BR> rc\_T68878\_f\_at T68878 3191 carboxylesterase 1 (monocyte/macrophage 60.35 down 0.00409<BR> rc\_T69009\_s\_at T69009 3192 quinoid dihydropteridine reductase 6.54 down 0.00145<BR> rc\_T69020\_at T69020 3193 EST 5.39 down 0.00383<BR> rc\_T69029\_f\_at T69029 3194 haptoglobin 33.18 down 0.02825<BR> rc\_T69164\_at T69164 3195 EST 4.38 down 0.00548<BR> rc\_T69284\_s\_at T69284 3196 mannose-binding lectin (protein C) 2, soluble 36.53 down 0<BR> T69384\_at T69384 3198 period (Drosophila) homolog 1 5.88 down 0.01219<BR> rc\_T69728\_at T69728 3199 heat shock 90kD protein 1, beta 3.98 down 0.00786<BR> rc\_T70087\_at T70087 3200 EST 4.7 down 0.00173<BR> rc\_T71012\_s\_at T71012 3201 fibrinogen, B beta polypeptide 43.61 down 0.00743<BR> rc\_T71021\_at T71021 3202 EST 6.74 down 0.0017<BR> rc\_T71373\_at T71373 3203 EST 83.08 down 0.00069<BR> rc\_T71776\_at T71776 3204 EST 10.3 down 0.00897<BR> rc\_T71978\_at T71978 3205 EST 4.39 down 0.0017 Table 6B.

Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_T72171\_s\_at T72171 3206 thyroxine-binding globulin 10.41 down 0.00163<BR> rc\_T72268\_s\_at T72268 3207 B-factor, properdin 7.43 down 0.01197<BR> rc\_T72502\_at T72502 3208 EST 8.87 down 0.00009<BR> rc\_T72629\_i\_at T72629 3209 EST 3.24 down 0.00556<BR> rc\_T72906\_at T72906 3210 EST 7.56 down 0.00062<BR> rc\_T73420\_at T7420 3211 short-chain dehydrogenase/reductase 1 4.58 down 0.00656<BR> rc\_T73433\_s\_at T73433 3212 angiotensinogen 48.3 down 0.00049<BR> rc\_T73442\_at T73442 3213 EST 94.41 down 0<BR> alanine-glyoxylate aminotransferase (oxalosis I);<BR> rc\_T73739\_s\_at T73739 3214 hyperoxaluria I; glycolicaciduria; serine-pyruvate 16.18 down 0.00277<BR> rc\_T74542\_s\_at T74542 3215 UDP glycosyltransferase 2 family, polypeptide 32.36 down 0.00004<BR> rc\_T74608\_at T74608 3216 hydroxyacid oxidase (glycolate oxidase) 1 14.03 down 0<BR> rc\_T74884\_r\_at T74884 3217 EST 3.76 down 0.02547<BR> rc\_T77729\_f\_at T77729 3218 pyruvate carboxylase 7.29 down 0.00022<BR> rc\_T78433\_s\_at T78433 3220 glycogen synthase 2 (liver) 8.62 down 0.00072<BR> rc\_T78889\_s\_at T78889 3221 fibronectin 1 19.87 down 0.00912<BR> rc\_T79758\_at T79758 3224 EST 3.94 down 0.00581<BR> rc\_T79842\_at T79842 3225 EST 3.16 down 0.03159<BR> rc\_T79863\_at T79863 3226 EST 5.62 down 0.00074<BR> rc\_T81315\_at T81315 3227 EST 4.28 down 0.00187<BR> rc\_T82254\_at T82254 3229 EST 3.82 down 0.00091<BR> rc\_T82259\_at T82259 3230 EST 3.12 down 0.01122<BR> rc\_T82323\_at T82323 3231 immunoglobulin superfamily, member 4 10.14 down 0<BR> rc\_T83356\_s\_at T83356 3232 apolipoprotein H (beta-2-glycoprotein I) 64.34 down 0.00802<BR> T83397\_at T83397 3233 phytanoyl-CoA hydroxylase (Refsum disease) 63.6 down 0<BR> T85532\_f\_at T85532 3236 EST 4.33 down 0.00591<BR> rc\_T86464\_at T86464 3237 EST 3.17 down 0.00498<BR> rc\_T86482\_at T86482 3238 transferrin 11.15 down 0.00006<BR> rc\_T86978\_s\_at T86978 3239 glutamate dehydrogenase 1 9.44 down 0.00006<BR> rc\_T87174\_at T87174 3240 EST 21.71 down 0.00681<BR> rc\_T90037\_at T90037 3246 EST 3.99 down 0.0016 Table 6B.

Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_T90492\_at T90492 3248 EST 3.88 down 0.00454<BR> rc\_T90520\_at T9052 3249 EST 8.67 down 0.00072<BR> rc\_T90531\_at T90531 3250 EST 3.6 down 0.00301<BR> rc\_T90841\_f\_at T90841 3251 EST 5.74 down 0.01876<BR> rc\_T91161\_at T91161 3253 EST 3.48 down 0.00002<BR> rc\_T91348\_at T91348 3254 EST 3.57 down 0.00011<BR> rc\_T92950\_at T92950 3256 EST 3.01 down 0.00497<BR> rc\_T94862\_at T94862 3258 EST 3.07 down 0.01417<BR> rc\_T95064\_at T95064 3260 EST 5.75 down 0.00604<BR> rc\_T95515\_s\_at T95515 3261 KIAA0249 gene product 6.77 down 0.0001<BR> T95813\_f\_at T95813 3262 KIAA1051 protein 38.38 down 0.00008<BR> rc\_T96969\_at T96969 3264 EST 3.42 down 0.00053<BR> rc\_T97234\_at T97234 3265 EST 4.34 down 0.00263<BR> rc\_T98199\_i\_at T98199 3267 EST 4.86 down 0.00431<BR> rc\_T98676\_at T98676 3269 EST 46.94 down 0.0001<BR> rc\_T99636\_s\_at T99636 3271 complement component 3 29.6 down 0.00051<BR> U00115\_at U00115 3272 B-cell CLL/lymphoma 6 (zinc finger protein 51) 5.18 down 0.00045<BR> glucose-6-phosphatase, catalytic (glycogen<BR> U01120\_at U01120 3274 storage disease type I, von Gierke disease) 13.41 down 0.00147<BR> solute carrier family 1 (glial high affinity glutamate<BR>

U01824\_at U01824 3276 transporter), member 2 3.2 down 0.00021<BR> U02020\_at U02020 3277 pre-B-cell colony-enhancing factor 3.37 down 0.01112<BR> U02388\_at U02388 3278 cytochrome P450, subfamily IVF, polypeptide 2 9.38 down 0.00001<BR> U03056\_at U03056 3280 hyaluronoglucosaminidase 1 6.64 down 0<BR> U03105\_at U03105 3281 proline-rich protein with nuclear targeting signal 4.69 down 0.00017<BR> ald-keto reductase family 1, member C1<BR> (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-<BR> U05861\_at U05861 3285 ydroxysteroid dehydrogenase) 23.22 down 0.00002<BR> U06641\_s\_at U06641 3287 UDP glycosyltrasferse 2 family, polypeptide 24.32 down 0.00001<BR> U06863\_at U06863 3288 follistatin-like 1 3.09 down 0.000091<BR> U08006\_s\_at U08006 3290 complement component 8, alpha polypeptide 16 down 0.00111 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> U08198\_rna1\_at U08198 3292 complement component 8, gamma polypeptide 19.71 down 0<BR> U08854\_s\_at U08854 3293 UDP glycosyltransferase 2 family, polypeptide 7.38 down 0.00005<BR> U11313\_at U11313 3297 sterol carrier protein 2 5.44 down 0.00187<BR> U12778\_at U12778 3301 acyl-Coenzyme A dehydrogenase, 5.68 down 0.00116<BR> sulfotransferase family 2A,<BR> U13061\_rna1\_at U13061 3302 dehydroepiandrosterone (DHEA) -preferring, 11.32 down 0.00048<BR> U16660\_at U16660 3313 enoyl Coenzyme A hydratase 1, peroxisomal 3.96 down 0.00002<BR> U19495\_s\_at U19495 3319 stromal cell-derived factor 1 4.59 down 0.00011<BR> U19523\_at U19523 3320 GTP cyclohydrolase 1 (dopa-responsive 5.25down 0.00029<BR> U20530\_at U20530 3322 secreted phosphoprotein 2, 24kD 16.93 down 0<BR> U20938\_at U20938 3324 dihydropyrimidine dehydrogenase 3.92 down 0.00053<BR> U21931\_at U21931 3326 fructose-bisphosphatase 1 3.4 down 0.00709<BR> cytochrome P450, subfamily IIA (phenobarbital-<BR> U22029\_f\_at U22029 3327 inducible), polypeptide 7 71.98 down 0<BR> U22961\_s\_at U22961 3330 albumin 22.22 down 0.01531<BR> aldehyde dehydrogenase 4 (glutamate gamma-<BR> U24266\_at U24266 3331 semialdehyde dehydrogenase; pyrroline-5- 14.54 down 0<BR> U25182\_at U25182 3333 trioredoxin peroxidase (antioxidant enzyme) 3.13 down 0.02543<BR> U26173\_s\_at U26173 3335 nuclear factor, interleukin 3 regulated 6.4 down 0.00001<BR> U27460\_at U27460 3339 UDP-glucose pyrophosphorylase 2 11.46 down 0.00088<BR> solute carrier family 6 (neurotransmitter<BR> U27699\_at U27699 3340 transporter, betaine/GABA), member 12 3.65 down 0.00381<BR> U28838\_at U28833 3341 Down syndrome candidate region 1 3.3 down 0.00306<BR> U29953\_rna1\_at U29953 3342 pigment epithelium-derived factor 15.33 down 0.00212<BR> U31449\_at U31449 3345 transmembrane 4 superfamily member 4 11.53 down 0.00187<BR> U32576\_rn1\_at U32576 3347 apolipoprotein C-IV 18.59 down 0.00005<BR> U32576\_rn1\_at U32576 3347 apolipoprotein C-IV 5.81 down 0.04343<BR> U32989\_at U32989 3348 tryptophan 2,3-dioxygenase 10.07 down 0.02825<BR> aldehyde dehydrogenase 9 (gamma-<BR> U34252\_at U34252 3350 aminobutyraldehyde dehydrogenase, E3 4.31 down 0.00613<BR> U36922\_at U36922 3352 EST 3.06 down 0.01388 Table 6B. Down regulated in metastatic canvers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> macrophage stimulating 1 (hepatocyte growth<BR> U3055\_ma1\_s\_at U37055 3353 factor-like), macrophages stimulating, pseudogene 18.28 down 0<BR> U44111\_at U44111 3363 histamine N-methyltransferase 3.5 down 0.00942<BR> U46499\_at U46499 3365 microsomal glutathione S-transferase 1 4.27 down 0.00244<BR> U46689\_at U46689 3366 aldehyde dehydrogenase 10 (fatty aldehyde 3.5 down 0.01292<BR> U48296\_at U48296 3369 protein tyrosine phosphatase type IVA, member 1 4.25 down 0.02037<BR> U48707\_at U48707 3371 protein phosphatase 1, regulatory (inhibitor) 14.22 down 0<BR> U48959\_at U48959 3372 myosin, light polypeptide kinase 3.61 down 0.00084<BR> U49082\_at U49082 3373 transporter protein 9.17 down 0.00088<BR> U49248\_at U49248 3374 ATP-binding cassette, sub-family C (CFTR/MRP), 7.06 down 0.00067<BR> U49352\_at U49352 3375 2,4-dienoyl CoA reductase 1, mitochondrial 5.41 down 0.02371<BR> U49785\_at U49785 3376 D-dopachrome tautomerase 3.84 down 0.00044<BR> U50196\_at U50196 3377 adenosine kinase 3.82 down 0.1425<BR> U50527\_s\_at U50527 3378 EST 3.93 down 0.00123<BR> U50929\_at U50929 93380 betaine-homocysteine methyltransferase 36.91 down 0<BR> Ut1010\_s\_at U51010 3381 nicotinamide N-methyltransferase 27.79 down 0.00366<BR> U51333\_s\_at U51333 3383 hexokinase 3



(white cell) 4.88 down 0.00055<BR> U51903\_at U51903 3387 IQ motif containing GTPase activating protein 2 3.23 down 0.00242<BR> U53003\_at U53003 3388 ES1 (zebrafish) protein, human homolog of 4.84 down 0.00077<BR> U56814\_at U56814 3393 deoxyribonuclease I-like 3 29.43 down 0.00003<BR> U56814\_at U56814 3393 deoxyribonuclease I-like 3 11.36 down 0.00001<BR> U57721\_at U57721 3395 kynureninase (L-kynurenine hydrolase) 4.34 down 0.0197<BR> U60205\_at U60205 3401 sterol-C4-methyl oxidase-like 5.16 down 0.00061<BR> U62389\_at U62389 3402 isocitrate dehydrogenase 1 (NADP+), soluble 3.15 down 0.03949<BR> U66674\_at U66674 3408 ATP-binding cassette, sub-family C (CFTR/MRP), 6.13 down 0.00127<BR> U67963\_at U67963 3410 lysophospholipase-like 3.19 down 0.00029<BR> U68233\_at U68233 3412 nuclear receptor subfamily 1, group H, member 4 6.76 down 0.00022<BR> U68494\_at U68494 3413 EST 4.82 down 0.00881<BR> U69141\_at U69141 3414 glutaryl-Coenzyme A dehydrogenase 3.06 down 0.00053<BR> U70732\_mal\_at U70732 3415 glutamic-pyruvate transaminase (alanine 27.63 down 0<BR> U70732\_mal\_at U70732 3415 glutamic-pyruvate transaminase (alaine 5.64 down 0.00146 Table 6B, Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> U73514\_at U73514 3419 hydroxyacyl-Coenzyme A dehydrogenase, type II 3.79 down 0.01392<BR> U73682\_at U73682 3420 meningioma expressed antigen 6 (coiled-coil 3.08 down 0.01249<BR> U76376\_at U76376 3425 karkiri, BCL2-interacting protein (contains only 11.77 down 0.00002<BR> U77396\_at U77396 3426 LPS\_induced TNF-alpha factor 4.47 down 0.00108<BR> U77594\_at U77594 3428 retinoic acid receptor responder (tazarotene 11.95 down 0.00527<BR> U78190\_mal\_at U78190 3431 GTP cyclohydrolase 1 feedback regulator protein 3.94 down 0.034<BR> U79294\_at U79294 3435 Phosphatidic acid phosphatase type 2b 3.13 down 0.00129<BR> U79303\_at U79303 3436 protein predicted by clone 23882 4.45 down 0<BR> U79716\_at U79716 3437 reelin 3.51 down 0.00053<BR> solute carrier family 9 (sodium/hydrogen<BR> U82108\_s\_at U82108 3441 exchanger), isoform 3 regulatory factor 2 3.19 down 0.01545<BR> U82468\_at U82468 3442 tubby like protein 1 3.34 down 0.0097<BR> U84569\_at U84569 3445 chromosome 21 open reading frame 2 3.46 down 0.01844<BR> U86529\_at U86529 3451 glutathione S-transferase zeta 1 3.41 down 0.0118<BR> U90544\_at U90544 3454 solute carrier family 17 (sodium phosphate), 6.42 down 0.00023<BR> U90545\_at U90545 3455 solute carrier family 17 (sodium phosphate), 4.14 down 0.00005<BR> U95090\_at U95090 3464 nephrosis 1, congenital, Finnish type (nephron) 14.01 down 0.00018<BR> U95090\_at U95090 3464 nephrosis 1, congenital, Finnish type (nephron) 7.44 down 0.00004<BR> W03796\_at W03796 3468 EST 8.3 down 0.0032<BR> W07723\_at W07723 3471 EST 3.51 down 0.00026<BR> rc\_W15528\_at W15528 3475 EST 3.56 down 0.00424<BR> W20094\_at W20094 3477 DKFZP586A0522 protein 38.09 down 0.00188<BR> W20276\_f\_at W20276 3478 EST 3.82 down 0.00033<BR> rc\_W20467\_f\_at W20467 3480 EST 7.76 down 0.00008<BR> W26769\_at W26769 3483 CGI-86 protein 8.14 DOWN 0.00204<BR> W26996\_AT W26996 3484 EST 6.42 down 0.00005<BR> W27023\_at W27023 3485 neuroendocrine-specific protein C like (foocen) 6.79 down 0.00805<BR> W28798\_at W28798 3492 phosphodiesterase 6A, cGMP-specific, rod, alpha 7.01 down 0.00017<BR> W28824\_at W28824 3493 EST 15.8 down 0.00006<BR> W28944\_at W28944 3494 EST 37.07 down 0.00205<BR> rc\_W31478\_s\_at W31478 3496 EST 3.36 down 0.01511 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_W33167\_at W22167 3499 EST 8.01 down 0.00026<BR> W35309\_at W35309 3500 EST 3.11 down 0.029<BR> W36290\_s\_at W36290 3501 Kreisler (mouse) maf-related leucine zipper 3.94 down 0.02718<BR> rc\_W37382\_at W37382 3502 EST 4.37 down 0.00677<BR> rc\_W38407\_at W38407 3506 EST 4.17 down 0.00392<BR> rc\_W42483\_at W42483 3510 EST 3.04 down 0.02518<BR> rc\_W42789\_at W42789 3515 EST 9.38 down 0.00059<BR> rc\_W42996\_at W42996 3517 EST 6.18 down 0.00587<BR> rc\_W44745\_at W44745 3520 EST 9.02 down 0.00276<BR> rc\_W45051\_at W45051 3521 EST 4.68 down 0.00433<BR> W45259\_at W45259 3522 EST 3.78 down 0.0069<BR> rc\_W45560\_at W45560 3525 EST 5.06 down 0.00996<BR> rc\_W46391\_at W46391 3527 alpha integrin binding protein 63 4.03 down 0.01363<BR> rc\_W46404\_at W46404 3528 EST 3.73 down 0.00116<BR> rc\_W47175\_at W47175 3534 3-prime-phosphoadenosine 5-prime- 5.54 down



0.00914<BR> rc\_W51951\_s\_at W51951 3542 dCMP deaminase<BR> CD36 antigen (collagen) type I receptor,<BR> W52581\_at W52581 3543 thrombospondin receptor)-linke 2 (lysosomal 3.08 down 0.00091<BR> W52821\_at W52821 3544 leucine aminopeptidase 4.02 down 0.03787<BR> W55903\_at W55903 3546 adipose differentiation-related protein; adipophilin 9.12 down 0.00459<BR> rc\_W57821\_at W57821 3548 EST 5.03 down 0.00277<BR> W58540\_AT W58540 3553 KIAA1131 protein 4.28 down 0.0184<BR> rc\_W58756\_at W58756 3554 EST 17.17 down 0.00087<BR> rc\_W60002\_s\_at W60002 3555 plastin 3 (T isoform) 4.88 down 0.01694<BR> rc\_W60186\_at W60186 3557 EST 3.24 down 0.00228<BR> rc\_W61000\_at W61000 3560 EST 3.15 down 0.03143<BR> rc\_W61319\_at W61319 3561 EST 3.02 down 0.00031<BR> W61377\_at W61377 356 EST 9.33 down 0.0012<BR> rc\_W61378\_s\_at W61378 3563 EST 8.31 down 0<BR> rc\_W63728\_at W63728 3565 EST 5.03 down 0.00311<BR> rc\_r63785\_at W63785 3567 EST 3.91 down 0.04089 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_W67147\_at W67147 3568 deleted in liver cancer 1 9.74 down 0.0002<BR> rc\_W67199\_at W67199 3569 EST 3.09 down 0.01528<BR> rc\_W67564\_s\_at @67564 3571 nuclear receptor subfamily, group B, member2 30.34 down 0<BR> rc\_W68721\_f\_at W68721 3572 cleft lip and palate associated transmembrane 6.34 own 0.01504<BR> rc\_W69675\_at W69675 3575 EST 4.42 down 0.00019<BR> rc\_W70115\_s\_at W70115 3576 histidine ammonia-lyase 1165 down 0.0003<BR> rc\_w70313\_at W70313 3578 EST 3 down 0.00643<BR> rc\_W72044\_at W72044 3580 insulin induced gene 1 24.58 down 0.00001<BR> rc\_W72079\_at W72079 3581 EST 6.36 down 0.00641<BR> rc\_W72972\_at W72972 3587 EST 5.61 down 0.00939<BR> rc\_W73194\_at W73194 3590 dermatopontin 3.45 Down 0.02211<BR> rc\_W73601\_at W73601 3592 EST 32.25 down 0<BR> rc\_W73818\_at W73818 3593 EST 4.32 down 0.00385<BR> rc\_W73889\_s\_at W73889 3594 tetranectin (plasminogen-binding protein 7.46 down 0.00091<BR> W74158\_at W74158 3596 EST 4.81 down 0.00091<BR> W79046\_at @79046 3602 peroxisomal D3,D2-enoyl-CoA isomerase 27.9 down 0.00023<BR> rc\_W79422\_s\_at W79422 3604 fumarylacetoacetate 14.92 down 0.00059<BR> rc\_W80609\_at W80609 3606 EST 4.68 down 0.01729<BR> W81053\_at W81053 3610 EST 4.91 down 0.00164<BR> rc\_W81079\_at W81079 3611 EST 3.31 down 0.0167<BR> protein kinase, interferon-inducible double<BR> W81268\_at W81268 3612 stranded RNA depdnt 4.2 down 0.00007<BR> rc\_W85765\_at W85765 3616 EST 3.83 down 0.00379<BR> rc\_W85847\_at W85847 3619 EST 7.28 down 0.00024<BR> rc\_W85886\_at W85886 3621 EST 3.46 down 0.00814<BR> rc\_W85888\_at W85888 3622 EST 3.99 down 0.00697<BR> rc\_W86075\_at W86075 3624 est 13.83 down 0.00697<BR> rc\_W86375\_s\_at W86375 3626 EST 19.29 down 0.0061<BR> rc\_W86431\_s\_at W86431 3627 protein C inhyibitor (plasminogen activgator inhibitor 14.94 down 0.00152<BR> rc\_W86600\_at W86600 3628 EST 32.14 down 0<BR> rc\_W86756\_at W86756 3630 retinoid receptor, alpha 3.77 down 0.2472 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> solute carrier family 25 (mitochondrial carrier;<BR> rc\_W86850\_f\_at W86850 3631 citrate trnsporter), ember 1 4.9 down 0.03105<BR> rc\_W87454\_at W87454 3632 homogentisate 1,2-dioxygenase (homogentisate 7.93 down 0.00149<BR> rc\_W87480\_at W87480 3633 STAT induced STAT inhibitor-2 3.24 down 0.01063<BR> rc\_w87532\_at W87532 3634 putative glycine-N-acyltransferase 12.34 down 0.00014<BR> rc\_W87606\_s\_at W87606 3635 protein Z, vitamin K-dependent plasma 9.23 down 0.00085<BR> rc\_W8778\_at W87781 3636 EST 6.1 down 0.00045<BR> rc\_w87824\_at W87824 3637 EST 3.67 down 0.01559<BR> rc\_W8568\_at W88568 3638 glycogenin 2 4.16 down 0.00111<BR> rc\_W88946\_at W88946 3639 putative glycine-N-acyltransferase 58.26 down 0<BR> rc\_W88985\_at W88985 3640 KIAA0903 protein 3.94 down 0.00295<BR> rc\_W89178\_at W89178 3641 transferrin receptor 2 10.85 down 0.00116<BR> rc\_W90128\_s\_at W90128 3643 X-box binding protein 1 10.04 down 0.00018<BR> rc\_W90455\_s\_at W90455 3646 alpha-2-macroglobulin 10.35 down 0.00063<BR> rc\_W90560\_at W90560 3647 EST 3.35 down 0.00388<BR> rc\_W90583\_r\_at W90583 3648 EST 3.435 down 0.00318<BR> rc\_W90766\_at W90766 3649 EST 7.58 DOWN 0.00057<BR> rc\_W92148\_s\_at W92148 3650 kininogen 51.09 down 0.00376<BR> rc\_W92713\_at W92713 3654 EST 16.55 down 0.00097<BR> rc\_W92771\_s\_at W92771 3655 glycine cleavage system protein H (aminomethyl 4.36

down 0.0064<BR> rc\_W94427\_at W94427 3659 EST 3.86 down 0.02649<BR> rc\_W94942\_i\_at W94942 3661 dual specificity phosphatase 10 7.23 down 0.00137<BR> rc\_W95041\_at W95041 3662 EST 12.79 down 0.00001<BR> W95795\_at W95795 3665 EST 7.8 down 0.00359<BR> X00129\_at X00129 367 retinol-binding protein 4, interstitial 18.57 down 0.02378<BR> AFFX-HSAC07/X00351\_M\_st X00351 3668 actin, beta 4.76 down 0.0003<BR> X01038\_mal\_s\_at X01038 3669 apolipoprotein A-I, apolipoprotein C-III 19.97 down 0.0275<BR> X01388\_at X01388 3670 apolipoprotein C-III 10.9 down 0.01246<BR> X02160\_at X02160 3671 insulin receptor 5.29 down 0.0001<BR> X02160\_at X02160 3671 insulin receptor 3.27 down 0.0007<BR> X02176\_s\_at X02176 3672 complement component 9 9.61 down 0.00004 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> X02750\_at X02750 3673 protein C (inactivator of coagulation factors Va 7.04 down 0.00079<BR> vitronectin (serum spreading factor, somatomedin<BR> X03168\_at X03168 3674 B, complement S-protein) 25.88 down 0.00911<BR> X03350\_at X03350 3676 alcohol dehydrogenase 2 (class I), beta 19.32 down 0.00001<BR> X04085\_mal\_at X04085 3678 catalase 11.27 down 0.0002<BR> gap junction protein, beta 1, 32kD (connexin 32,<BR> X04325\_at X04325 3679 Charcot-Marie-Tooth neuropathy, X-linked) 10.17 down 0.00061<BR> X04729\_s\_at X04729 3682 plasminogen activator inhibitor, type I 3.15 down 0.01337<BR> guanine nucleotide binding protein (G protein),<BR> X04828\_at X04828 3683 alpha inhibiting activity polypeptide 2 5.22 down 0.01278<BR> X05409\_at X05409 3684 aldehyde dehydrogenase 2, mitochondrial 3.99 down 0.01029<BR> X06562\_at X06562 3686 growth hormone receptor 10.87 down 0.00001<BR> X07173\_at X07173 3690 inter-alpha (globulin) inhibitor, H2 polypeptide 30.3 down 0.00016<BR> cytochrome P450, subfamily IID (debrisoquine,<BR> X07618\_s\_at X07618 3691 sparteine, etc., -metabolising), polypeptide 7a 35.79 down 0.00065<BR> cytochrome P450, subfamily IID (debrisoquine,<BR> X07618\_s\_at X07618 3691 sparteine, etc., -metabolising), polypeptide 7a 13.58 down 0<BR> cytochrome P450, subfamily IID (debrisoquine,<BR> X07619\_s\_at X07619 3692 sparteine, etc., -metabolising), polypeptide 7a 4.96 down 0.00004<BR> X07732\_at X07732 3693 hepsin (transmembrane protease, serine 1) 28.21 down 0<BR> X07767\_at X07767 3694 protein kinase, cAMP-dependent, catalytic, alpha 5.94 down 0.00028<BR> X12662\_mal\_at X12662 3697 arginase, liver 20.59 down 0<BR> X13227\_at X13227 3698 D-amino-acid oxidase 4.81 down 0.0002<BR> X13334\_at X13334 3699 CD14 antigen 12.77 down 0.00887<BR> cytochrome P450, subfamily IIA (phenobarbital-<BR> X13930\_f\_at X13930 3700 inducible), polypeptide 6 38.52 down 0<BR> X14690\_s\_at X14690 3703 pre-alpha (globulin) inhibitor, H3 polypeptide 16.07 down 0.00438<BR> X14787\_at X14787 3704 thrombospondin 1<BR> acetyl-Coenzyme A acyltransferase 1<BR> X14813\_at X14813 3705 (peroxisomal 3-oxoacyl-Coenzyme A thiolase) 11.61 down 0.0002<BR> X15422\_at X15422 3708 mannose-binding lectin (protein C) 2, soluble 8.29 down 0.00015 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> X16260\_s\_at X16260 3710 inter-alpha (globulin) inhibitor, H1 polypeptide 44.65 down 0.00933<BR> X16260\_s\_at X16260 3710 inter-alpha (globulin) inhibitor, H1 polypeptide 26.39 down 0.0004<BR> X16349-s\_at X16349 3712 sex hormone-binding globulin 9.34 down 0.00007<BR> X17025\_at X17025 3715 isopentenyl-diphosphate delta isomerase 3.13 down 0.0043<BR> paired basic amino acid cleaving enzyme (furin,<BR> X17094\_at X17094 3717 membrane associated receptor protein) 8.5 down 0<BR> X52150\_mal\_s\_at X52150 3722 arylsulfatase A 3.51 down 0.00113<BR> X52520\_at X52520 3723 tyrosine aminotransferase 13.51 down 0.00002<BR> X52541\_at X52541 3724 early growth response 1 3.77 down 0.00894<BR> alanine-glyoxylate aminotransferase (oxalosis I;<BR> X53414\_at X53414 3728 hyperoxaluria I; glycolicaciduria; serine-pyruvate 13.87 down 0.00003<BR> X53595\_s\_at X53595 3729 apolipoprotein H (beta-2-glycoprotein I) 27.28 down 0.0066<BR> X54380\_at X54380 3730 pregnancy-zone protein 8.44 down 0.00059<BR> X55283\_mal\_s\_at X55283 3734 asialoglycoprotein receptor 2 84.99 down 0.00084<BR> X56411\_mal\_at X56411 3737 alcohol dehydrogenase 4 (class II), pi polypeptide 25.14 down 0.00144<BR> X56692\_at X56692 3739 C-reactive protein, pentraxin-related 15.15 down 0.01884<BR> X57025\_at X57025 3742 insulin-like growth factor 1 (somatomedin C) 4.72 down 0.00087<BR> X58022\_at X58022 3747 corticotropin

releasing hormone-binding protein 4.09 down 0.00076<BR> X58528\_s\_at X58528 3748 ATP-binding cassette, sub-family D (ALD), 4.91 down 0.00728<BR> X59766\_at X59766 3749 alpha-2-glycoprotein 1, zinc 12.96 down 0.0004<BR> cytochrome P450, subfamily XXVIIA (steroid 27-<BR> X59812\_at X59812 3750 hydroxylase, cerebrotendinous xanthomatosis), 4.65 down 0.036<BR> X59834\_at X59834 3751 glutamate-ammonia ligase (glutamine synthase) 4.29 down 0.00255<BR> X60673\_s\_at X60673 3752 adenylate kinase 3 8.3 down 0.00016<BR> X61123\_at X61123 3753 B-cell translocation gene, 1 anti-proliferative 3.2 down 0.00796<BR> X62822\_at X62822 3758 sialyltransferase 1 (beta-galactoside alpha-2,6- 4.89 down 0.00274<BR> X63359\_at X63359 3759 UDP glycosyltransferase 2 family, polypeptide 13.66 down 0.00051<BR> X64877\_at X64877 3766 H factor (complement)-like 3 14.6 down 0<BR> X64877\_s\_at X64877 3766 H factor (complement)-like 3 12.33 down 0<BR> X65727\_cds\_s\_at X65727 3768 glutathione S-transferase A2, glutathione S- 73.64 down 0<BR> X65962\_s\_at X65962 3769 cytochrome P450, subfamily IIC (mephenytoin 4- 5.47 down 0.00014 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> X67235\_s\_at X67235 3773 hematopoietically expressed homeobox 3.17 down 0.0045<BR> X67491\_f\_at X67491 3776 glutamate dehydrogenase 1 7.45 down 0.00019<BR> X68277\_at X68277 3777 dual specificity phosphatase 1 6.68 down 0.0036<BR> X68679\_s\_at X68679 3779 complement factor H related 3, complement factor 38.22 down 0.00036<BR> X68733\_ma1\_at X68733 3781 alpha-1-antichymotrypsin 7.87 down 0.03266<BR> X72012\_at X72012 3789 endoglin (Osler-Rendu-Weber syndrome 1) 4.2 down 0.005<BR> X72177\_ma1\_at X72177 3790 complement component 6 12.94 down 0.00011<BR> X75252\_at X75252 3793 prostatic binding protein 3.78 down 0.00231<BR> X76105\_at X76105 3794 death-associated protein 3.02 down 0.00944<BR> X76648\_at X76648 3796 glutaredoxin (thioltransferase) 4 down 0.00211<BR> X76717\_at X76717 3797 metallothionein 1L 8.09 down 0.00025<BR> X77548\_at X77548 3798 nuclear receptor coactivator 4 3.76 down 0.00758<BR> X78706\_at X78706 3801 carnitine acetyltransferase 4.65 down 0.00442<BR> X78992\_at X78992 3802 butyrate response factor 2 (EGF-response factor 4.69 down 0.01995<BR> prion protein (p27-30) (Creutzfeld-Jakob disease,<BR> X83416\_s\_at X83416 3811 Gerstmann-Strausler-Scheinker syndrome, fatal 3.28 down 0.00221<BR> 3-hydroxy-3-methylglutaryl-Coenzyme A synthase<BR> X83618\_at X83618 3813 2 (mitochondrial) 6.27 down 0.02099<BR> X85116\_ma1\_s\_at X85116 3814 erythrocyte membrane protein band 7.2 6.37 down 0.00356<BR> X86401\_s\_at X86401 3815 glycine amidinotransferase (L-arginine:glycine 22.7 down 0<BR> X87344\_cds10\_r\_at X87344 3817 EST 3.04 down 0.02779<BR> X95079\_s\_at X95079 3819 EST 29.82 down 0.00273<BR> X90999\_at X90999 3820 hydroxyacyl glutathione hydrolase; glyoxalase 2 5.27 down 0.00047<BR> X91148\_at X91148 3821 microsomal triglyceride transfer protein (large 5.91 down 0.00045<BR> X92720\_at X92720 3826 phosphoenolpyruvate carboxykinase 2 7.6 down 0.00001<BR> X92744\_at X92744 3827 defensin, beta 1 4.96 down 0.01804<BR> X94563\_xpt2\_r\_at X94563 3831 EST 3.52 down 0.00928<BR> X95190\_at X95190 3832 acyl-Coenzyme A oxidase 2, branched chain 12.81 down 0<BR> X95384\_at X95384 3833 translational inhibitor protein p14.5 17.69 down 0.00048<BR> X95715\_at X95715 3835 ATP-binding cassette, sub-family C (CFTR\_atMRP), 6.78 down 0.00045<BR> X95876\_at X95876 3836 G protein-coupled receptor 9 3.12 down 0.001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> X96752\_at X96752 3837 L-3-hydroxyacyl-Coenzyme A dehydrogenase, 4.94 down 0.00359<BR> X97324\_at X97324 3839 adipose differentiation-related protein; adipophilin 5.97 down 0.04638<BR> X98337\_s\_at X98337 3840 complement factor H related 3, complement factor 13.5 down 0.00001<BR> Y00097\_s\_at Y00097 3844 annexin A6 3.4 down 0.00233<BR> Y00317\_at Y00317 3845 UDP glycosyltransferase 2 family, polypeptide B4 18.34 down 0.00001<BR> Y00317\_at Y00317 3845 UDP glycosyltransferase 2 family, polypeptide B4 8.97 down 0.00025<BR> Y00318\_at Y00318 3846 I factor (complement) 10 down 0.00019<BR> Y00339\_s\_at Y00339 3847 carbonic anhydrase II 6.89 down 0<BR> Y00451\_s\_at Y00451 3848 aminolevulinate, delta-, synthase 1 10.52 down 0.00107<BR> Y08374\_ma1\_at Y08374 3853 chitinase 3-like 1 (cartilage glycoprotein-39) 3.5 down 0.04208<BR> Y08409\_at Y08409 3854 thyroid hormone responsive SPOT14 (rat) 5.84 down 0.00455<BR>

Y09616\_at Y09616 3857 carboxylesterase 2 (intestine, liver) 18.78 down 0.00026<BR> Y10032\_at  
 Y10032 3858 serum\_atglucocorticoid regulated kinase 4.24 down 0.00148<BR> Y10659\_at Y10659  
 3859 interleukin 13 receptor, alpha 1 4.22 down 0.00061<BR> Y01659\_at Y10659 3859 interleukin 13  
 receptor, alpha 1 3.17 down 0.00095<BR> Y12711\_at Y12711 3861 progesterone binding protein 14.83  
 down 0.00285<BR> Z11559\_at Z11559 3862 iron-responsive element binding protein 1 4.3 down  
 0.00066<BR> Z11737\_at Z11737 3863 flavin containing monooxygenase 4 3.84 down 0.00043<BR>  
 Z11737\_at Z11737 3863 flavin containing monooxygenase 4 3.67 down 0.00632<BR> Z11793\_at  
 Z11793 3864 selenoprotein P, plasma, 1 9.94 down 0.00021<BR> branched chain keto acid  
 dehydrogenase E1,<BR> Z14093\_at Z14093 3865 alpha polypeptide (maple syrup urine disease) 3.24  
 down 0.00301<BR> Z20777\_at Z20777 3866 EST 29.59 down 0.00044<BR> Z24459\_ma1\_at Z24459  
 3869 mature T-cell proliferation 1 5.29 down 0.00001<BR> Z24725\_at Z24725 3870 mitogen inducible  
 2 7.9 down 0<BR> Z26491\_s\_at Z26491 3873 catechol-O-methyltransferase 3.08 down 0.00877<BR>  
 aldo-keto reductase family 1, member D1 (delta 4-<BR> Z28339\_at Z28339 3875 3-ketosteroid-5-beta-  
 reductase) 24.66 down 0<BR> Z29481\_at Z29481 3877 3-hydroxyanthranilate 3,4-dioxygenase 6.39  
 down 0.00029<BR> Z29481\_at Z29481 3877 3-hydroxyanthranilate 3,4-dioxygenase 3.64 down  
 0.00096<BR> Z30425\_at Z30425 3878 nuclear receptor subfamily 1, group I, member 3 26.64 down 0  
 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.<BR> <P>Affy ID Genbank  
 Seq ID Known Gene Name Fold Change Direction Pvalue<BR> Z30425\_at Z30425 3878 nuclear  
 receptor subfamily 1, group I, member 3 7.88 down 0.000066<BR> Z31357\_at Z31357 3880 cystein  
 dioxygenase, type I 11.2 down 0.0001<BR> Z31690\_s\_at Z31690 3881 lipase A, lysosomal acid,  
 cholesterol esterase 3.83 down 0.00103<BR> rc\_Z38161\_at Z38161 3884 EST 4.38 down 0.0011<BR>  
 rc\_Z38192\_s\_at Z38192 3885 EST 3.35 down 0.00184<BR> rc\_Z38435\_at Z38435 3890 ribosomal  
 protein L21 3.12 down 0.03617<BR> rc\_Z38777\_f\_at Z38777 3895 nuclear receptor binding factor-2  
 3.28 down 0.022<BR> rc\_Z39059\_at Z39059 3899 EST 5.19 down 0.0014<BR> rc\_Z39406\_at Z39406  
 3905 nuclear receptor co-repressor 1 4.18 down 0.00439<BR> rc\_Z39431\_at Z39431 3907 KIAA1086  
 protein 3.68 down 0.0013<BR> rc\_Z39476\_at Z39476 3908 EST 5.9 down 0.00687<BR>  
 rc\_z39622\_s\_at Z39622 3910 EST 4.4 down 0.00001<BR> rc\_Z39818\_at Z39818 3912 EST 3.26 down  
 0.00089<BR> rc\_Z39833\_at Z39833 3913 GTP-binding protein 16.89 down 0.00034<BR>  
 rc\_Z39976\_at Z39976 3915 EST 5.76 down 0.00012<BR> rc\_Z39978\_at Z39978 3916 EST 3.56 down  
 0.04051<BR> rc\_Z40192\_at Z40192 3918 EST 3.89 down 0.00223<BR> rc\_Z40259\_s\_at Z40259  
 3919 EST 8.18 down 0.00002<BR> rc\_Z40305\_at Z40305 3920 EST 6.45 down 0.00001<BR>  
 rc\_Z40715\_at Z40715 3923 delta-6 fatty acid desaturase 18.68 down 0.0007<BR> rc\_Z40902\_at  
 Z40902 3926 SEC14 (S. cerevisiae)-like 2 12.87 down 0.00001<BR> rc\_Z41042\_at Z41042 3928 EST  
 3.63 down 0.00943<BR> Z47553\_at Z47553 3939 flavin containing monooxygenase 5 6.17 down  
 0.00011<BR> Z48199\_at Z48199 3942 syndecan 1 4.43 down 0.00408<BR> Z48475\_at Z48475 3943  
 glucokinase (hexokinase 4) regulatory protein 13.84 down 0<BR> Z49269\_at Z46269 3945 small  
 inducible cytokine subfamily A (Cys-Cys), 18.46 down 0.00001<BR> Z49878\_at Z49878 3946  
 guanidinoacetate N-methyltransferase 13.96 down 0.00021<BR> Z69923\_at Z69923 3948 HGF  
 activator 11.37 down 0.00053<BR> Z80345\_ma1\_s\_at Z80345 3951 acyl-Coenzyme A dehydrogenase,  
 C-2 to C-3 5.93 down 0.0024<BR> Z84718\_cds1\_at Z84718 3952 EST 3.26 down 0.02252<BR>  
 Z84721\_cds2\_at Z84721 3953 hemoglobin, zeta 8.77 down 0.01446 Table 7A. Up regulated in  
 hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene  
 Name Fold Change Direction Pvalue<BR> rc\_AA005358\_at AA005358 14 EST 5.51 down  
 0.00059<BR> rc\_AA007395\_s\_at AA007395 17 alcohol dehydrogenase 4 (class II), pi polypeptide  
 37.78 down 0.00939<BR> rc\_AA07629\_at AA07629 19 EST 5.56 down 0.0005<BR>  
 rc\_AA010205\_at AA010205 23 EST 5.71 down 0.00014<BR> rc\_AA010605\_s\_at AA010605 26 4-  
 hydroxyphenylpyruvate dioxygenase 25.52 down 0.00855<BR> rc\_AA010619\_at AA010619 27 EST  
 5.28 down 0.002<BR> rc\_AA018922\_s\_at AA018922 40 core promoter element binding protein 3.39  
 down 0.01801<BR> rc\_AA035245\_s\_at AA035245 79 aldehyde oxidase 1 7.97 down 0.02387<BR>  
 rc\_AA035457\_at AA035457 80 EST 3.41 down 0.00968<BR> rc\_AA039335\_s\_at AA039335 89  
 coagulation factor XII (Hageman factor) 5.33 down 0.03807<BR> rc\_AA039616\_at AA039616 90 EST

3.84 down 0.00997<BR> rc\_AA046457\_at AA046457 111 EST 3.05 down 0.02078<BR>  
rc\_AA046747\_at AA046747 114 EST 4.77 down 0.00023<BR> rc\_AA056482\_at AA056482 141 EST  
3.06 down 0.01313<BR> rc\_AA057678\_at AA057678 143 EST 6.63 down 0.00089<BR>  
rc\_AA069696\_at AA069696 150 EST 3.07 down 0.01569<BR> rc\_AA070191\_at AA070191 154 EST  
3.24 down 0.00216<BR> rc\_AA074885\_at AA074885 161 macrophage receptor with collagenous  
structure 10.88 down 0.00087<BR> rc\_AA076326\_at AA076326 170 SEC14 (S. cerevisiae)-like 2 3.85  
down 0.0349<BR> rc\_AA076383\_at AA076383 171 EST 4.65 down 0.00593<BR> rc\_aa084668\_at  
AA084668 180 ubiquitin-like 3 3.31 down 0.02055<BR> rc\_AA085987\_s\_at AA085987 183 UDP  
glycosyltransferase 1 4.74 down 0.03035<BR> AA090257\_at AA090257 190 superoxide dismutase 2,  
mitochondrial 3.03 down 0.02774<BR> AA090439\_at AA090439 192 ribosomal protein S6 5.11 down  
0.01108<BR> rc\_AA099225\_at AA099225 206 EST 6.59 down 0.00064<BR> rc\_AA100026μ  
AA10026 211 EST 4.18 down 0.00567<BR> rc\_AA112101\_f\_at AA112101 222 EST 4.36 down  
0.03175<BR> rc\_AA122345\_f\_at AA122345 238 glutamate dehydrogenase 1 3.75 down 0.01058<BR>  
rc\_AA129390\_at AA129390 262 EST 4.03 down 0.00128<BR> rc\_AA142849\_at AA142849 306 EST  
3.45 down 0.03495<BR> rc\_aa147646\_s\_at AA147646 317 DKFZP586A0522 protein 3.19 down  
0.00508 Table 7A.Up reglated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy  
ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA150776\_at  
AA150776 330 EST 6.17 down 0.0004<BR> rc\_AA151676\_at AA151676 337 peptidyl arginine  
deminase, type II 3.85 down 0.00875<BR> aldo-keto reductase famil6 7, member A2 (aflatoxin<BR>  
rc\_AA157799\_at AA157799 348 aldehyde reductase) 3.8 down 0.00207<BR> rc\_AA164586\_s\_at  
AA164586 359 estrogen receptor 1 3.56 down 0.01231<BR> rc\_AA167565\_at AA167565 362 EST  
3.81 down 0.04057<BR> rc\_AA172372\_at AA172372 370 EST 5.12 down 0.00032<BR>  
rc\_AA182030\_at AA182030 387 EST 3.51 down 0.0403<BR> AA188921\_at AA188921 393 similar to  
Caenorhabidits elegans protein C42C1.9 3.38 down 0.00862<BR> rc\_AA194997\_s\_at AA194997 412  
EST 4.8 down 0.00153<BR> rc\_AA196287\_at AA196287 420 EST 4.86 down 0.01656<BR>  
rc\_AA210850\_at A210850 431 EST 3.12 down 0.00288<BR> rc\_AA223902\_at AA223902 450 EST  
4.22 down 0.01315<BR> rc\_AA232114\_s\_at AA232114 463 epoxide hydrolase 2, cytoplasmic 6.18  
down 0.00231<BR> rc\_AA233152\_at AA233152 467 EST 5.8 down 0.00272<BR> rc\_AA233837\_at  
AA233837 474 EST 3.46 down 0.01365<BR> rc\_AA235310\_at AA235310 496 EST 7.08 down  
0.04056<BR> rc\_AA236401\_at AA236401 510 EST 5.31 down 0.01787<BR> rc\_AA236455\_r\_at  
AA236455 52 EST 6.73 down 0.02418<BR> rc\_AA236455\_s\_at AA236455 512 EST 5.1 down  
0.00307<BR> rc\_AA253216\_at AA253216 561 EST 4.14 down 0.0014<BR> rc\_AA253369\_s\_at  
AA253369 563 EST 5.64 down 0.00478<BR> rc\_AA256367\_s\_at AA256367 579 paraoxonase 3 8.37  
down 0.902326<BR> rc\_AA258350\_at AA258350 592 EST 4.1 down 0.02962<BR>  
rc\_AA279676\_s\_at AA27O676 630 deoxyribonuclease I-like 3 10.52 down 0.00181<BR>  
rc\_AA282061\_at AA282061 652 KIAA0962 protein 3.46 down 0.00025<BR> rc\_AA282886\_at  
AA282886 663 EST 3.29 down 0.00025<BR> rc\_AA284795\_at AA284795 678  
phosphatidylethanolamine N-methyltransferase 5.7 down 0.0004<BR> rc\_AA285053\_at AA285053  
681 EST 5 down 0.00718<BR> rc\_AA287122\_at AA287122 686 EST 5.21 down 0.00523<BR>  
rc\_AA287566\_at AA287566 690 K8IAA0187 gene product 6.99 down 0.00023 Table 7A.Up reglated  
in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known  
Gene Name Fold Change Direction Pvalue<BR> rc\_AA291749\_s\_at AA291749 703 estrogen receptor  
1 5.06 down 0.00044<BR> rc\_AA297532\_f\_at AA297532 725 down 5.01 down 0.00745<BR>  
rc\_AA343142\_at AA343142 751 EST 5.79 down 0.02747<BR> fatty-acid-Coenzyme A ligase, long-  
chain 1, fatty-acid-<BR> rc\_AA348922\_s\_at AA348922 758 Coenzyme A ligase, long0-chain 2 11.4  
down 0.00848<BR> AA376875\_at AA376875 770 monoamine oxidase A 3.45 down 0.00105<BR>  
rc\_AA377087\_at AA377087 771 3EST 4.61 down 0.01616<BR> AA397841\_at AA397841 780 EST  
3.29 down 0.00825<BR> rc\_AA398892\_at AA398892 800 similar to yeast BET3 (S. cerevisiae) 4.33  
down 0.01326<BR> AA400177\_at AA400177 808 EST 3.21 down 0.03901<BR> rc\_AA401376\_at  
AA401376 829 EST 3.39 down 0.01403<BR> rc\_AA401562\_s\_at AA401562 830 EST 7.97 down  
0.00527<BR> rc\_AA402224\_at AA402224 836 growth arrest and DNA-damage-inducible, gamma 3.66



down 0.0033<BR> rc\_AA404487\_at AA404487 851 EST 3.01 down 0.0059<BR> rc\_AA417046\_at AA417046 915 fatty-acid-Coenzyme A ligase, very long-chain 1 8.49 down 0.02476<BR> small inducible cytokine subfamily B (Cyx-X-Cys),<BR> rc\_AA426640\_at AA426640 969 member 14 (BRAK) 4.8 down 0.00539<BR> rc\_AA428325\_at AA428325 988 EST 4.09 down 0.02486<BR> rc\_AA433946\_at AA433946 1033 EST 10.24 down 0.00663<BR> rc\_AA435746\_f\_at AA435746 1043 GTPase activating protein-like 4.21 down 0.03192<BR> rc\_AA435985\_at AA435985 1049 EST 3.86 down 0.01713<BR> AA442334\_at AA442334 1069 EST 3.02 down 0.01936<BR> rc\_AA446864\_at AA446864 1095 EST 11.57 down 0.0001<BR> rc\_AA448002\_at AA448002 1113 putative type II membrane protein 14.14 down 0<BR> FXD domain-containing ion transport regulator 1<BR> rc\_AA448300\_at AA448300 1116 (phospholemman) 9.27 down 0.00108<BR> rc\_AA450114\_at AA450114 1131 EST 3.29 down 0.01171<BR> rc\_AA450127\_at AA450127 1132 growth arrest and DNA-damage-inducible, beta 3.37 down 0.00647<BR> rc\_AA453988\_at AA453988 1160 methionine adenosyltransferase I, alpha 7.78 down 0.02695<BR> rc\_AA454733\_s\_at AA454733 1169 EST 5.73 down 0.00748<BR> rc\_AA455367\_at AA455367 1176 DKFZP586F1018 protein 3.47 down 0.00138 Table 7A.Up regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> butyrobetaine (gamma), 2-oxoglutarate dioxygenase<BR> rc\_AA455988\_at AA455988 1184 (gamma-butyrobetaine hydroxylase) 12.51 down 0<BR> rc\_AA458652\_at AA458652 1202 EST 5.03 down 0.00065<BR> solute carrier family 22 (extraneuronal monoamine)<BR> rc\_AA460012\_at AA460012 1224 transporter, member 3 3.73 down 0.0313<BR> rc\_AA460449\_at AA460449 1228 EST 3.53 down 0.01247<BR> rc\_AA460661\_at AA460661 1229 EST 5.46 down 0.00151<BR> rc\_AA461444\_at AA461444 1239 EST 3.19 down 0.02844<BR> rc\_AA465233\_s\_at AA465233 1269 succinate-CoA ligase, GDP-forming, beta subunit 3.19 down 0.00036<BR> rc\_AA477119\_at AA477119 1289 EST 4.62 down 0.00072<BR> AA477919\_at AA477919 1293 EST 3.9 down 0.00265<BR> rc\_AA478298\_s\_at AA478298 1297 adipose specific 2 5.29 down 0.00943<BR> rc\_AA480991\_s\_at AA480991 1323 EST 4.83 down 0.03498<BR> AA486511\_at AA486511 1349 EST 3.9 down 0.0149<BR> rc\_AA490620\_at AA490620 1378 EST 6.25 down 0.03613<BR> rc\_AA599472\_at AA599472 1451 succinate-CoA ligase, GDP-forming, beta subunit 3.31 down 0.02619<BR> rc\_AA599814\_at AA599814 1456 EST 4.09 down 0.00235<BR> rc\_AA599937\_s\_at AA599937 1458 insulin-like growth factor-binding protein 4 6.31 down 0.0477<BR> rc\_AA608802\_at AA608802 1470 EST 3.44 down 0.01709<BR> rc\_AA608837\_at AA608837 1472 EST 5.15 down 0.00005<BR> rc\_AA609519\_at AA609519 482 EST 5.23 down 0.00068<BR> rc\_AA609537\_s\_at AA609537 1483 hepatic leukemia factor 4.88 down 0.00118<BR> rc\_AA621131\_at AA621131 1513 EST 4.57 down 0.03867<BR> rc\_AA621209\_at AA621209 1516 similar to Caenorhabditis elegans proteinC42C1.9 4.01 down 0.00563<BR> C02386\_s\_at c02386 1561 hypothetical protein 3.66 down 0.0673<BR> C02460\_at C02460 1562 EST 3.92 down 0.03073<BR> rc\_C20653\_at C20653 1578 EST 4.32 down 0.00718<BR> rc\_C20810\_at C20810 1579 EST 3.57 down 0.02116<BR> rc\_C21130\_at C21130 1583 EST 3.24 down 0.03355<BR> cytochrome p450, subfamily IIA (naphthodiol oxidase),<BR> D00003\_at D00003 1586 polypeptide 3 9.46 down 0.00001 Table 7A.Up regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> cytochrome P450, subfamily IIA (naphthodiol oxidase),<BR> D00003\_s\_at D00003 1586 polypeptide 3 6.8 down 0.01328<BR> cytochrome P450, subfamily IIA (naphthodiol oxidase),<BR> polypeptide 3, cytochrome P450, subfamily IIA<BR> (naphthodiol oxidase), polypeptide 5, cytochrome P450,<BR> D00408\_s\_at D00408 1589 subfamily IIA, polypeptide 7 3.58 down 0.02048<BR> D10040\_at D10040 1593 fatty-acid-Coenzyme A ligase, longchain 2 4.15 down 0.02947<BR> rc\_D11756\_f\_at D11756 1596 EST 4.08 down 0.02972<BR> cytochrome P450, subfamily IVF, polypeptide<BR> 2, cytochrome P450, subfamily IVF, polypeptide 3<BR> D12620\_s\_at D12620 1601 (leukotriene B4 omega hydroxylase) 6.03 down 0.03947<BR> cytochrome p450, subfamily IVF, polypeptide<BR> 2, cytochrome p450, subfamily IVF, polypeptide 3<BR> D12620\_s\_at D12620 1601 (leukotriene B4 omega hydroxylase) 4.7 down 0.04091<BR> D13243\_s\_at D13243 1602 pyruvate kinase, liver and RBC 5.58 down 0.04029<BR> D13705\_s\_at D13705 1610 cytochrome P450, subfamily IVA, polypeptide 11 3.3 down



0.0051<BR> D14012\_s\_at D14012 1612 HGF activator 7.27 down 0.00145<BR> D1628\_s\_at D31628 1646 4hydroxyphenylpyruvate dioxygenase 13.18 down 0.02064<BR> rc\_D45529\_at D45529 1662 EST 3.01 down 0.03105<BR> D49357\_at D49357 1665 methionine adenosyltransferase I, alpha 4.85 down 0.04435<BR> rc\_D62518\_at D62518 1708 EST 5.96 down 0.00027<BR> ficolin (collagen/fibrinogen domain-containing lectin) 2<BR> D63160\_at D63160 1709 (hucolin) 3.72 down 0.00312<BR> D78011\_at D78011 1717 dihydropyrimidinase 5.54 down 0.0312<BR> D78725\_at D78725 1720 KIAA0914 gene product 3.19 down 0.01083<BR> D79276\_at D79276 1722 succinate-CoA ligase, GDP-forming, beta subunit 4.34 down 0.00836<BR> D90042\_at D90042 1767 N-acetyltransferase 2 (arylamine N-acetyltransferase) 3.79 down 0.00697<BR> rc\_F02028\_at F02028 1774 EST 3.15 down 0.00902<BR> rc\_F00245\_at F02245 1776 monomamine oxidase A 3.51 down 0.01692<BR> matrix metalloproteinase 2 (gelatinase A, 72kD<BR> rc\_F03969\_at F03969 1785 gelatinase, 72kD type IV collagenase) 3.36 down 0.01685 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_Ho2855\_at H02855 1832 EST 4.29 down 0.0138<BR> rc\_H05704\_s\_at H05704 1848 EST 3.07 down 0.00363<BR> rc\_H06935\_s\_at H06935 1855 electron-transferring-flavoprotein dehydrogenase 4.04 down 0.01498<BR> rc\_H08102\_at H08102 1858 breast cell glutaminase 12.85 down 0.0424<BR> rc\_H09317\_at H09317 1864 EST 3.2 down 0.00914<BR> methylenetetrahydrofolate dehydrogenase (NADP+<BR> dependent), methenyltetrahydrofolate cyclohydrolase,<BR> rc\_H10779\_s\_at H10779 1872 formyltetrahydrofolate synthetase 3.09 down 0.0496<BR> rc\_H20543\_at H20543 1897 DKFZP586B1621 protein 13.06 down 0.00218<BR> rc\_h27330\_at H27330 1909 EST 3.37 down 0.01318<BR> rc\_H29568\_at H29568 1914 EST 5 down 0.00426<BR> rc\_H55759\_at H55759 1949 EST 4.36 down 0.0398<BR> rc\_H57060\_s\_at H57060 1954 EST 7.57 down 0.0875<BR> rc\_H57816\_at H57816 1957 EST 3.09 down 0.01327<BR> rc\_H58673\_at H58673 1959 EST 15.49 down 0.00002<BR> rc\_h58692\_s\_at H58692 1960 formyltetrahydrofolate dehydrogenase 20.18 down 0.00485<BR> rc\_H59136\_at H59136 1962 EST 6.63 down 0.00033<BR> rc\_H62212\_at H62212 1969 telomeric repeat binding factor 2 3.23 down 0.00513<BR> H66367\_at H66367 1977 EST 3.84 down 0.00133<BR> rc\_H66840\_at H66840 1978 EST 3.34 down 0.01884<BR> rc\_H77597\_f\_at H77597 2000 metallothionein 1H 9.01 down 0.00022<BR> ficolin (collagen/fibrinogen domain-containing) 3 (H akata<BR> rc\_H80901\_s\_at H80901 2005 antigen) 18.59 down 0<BR> rc\_H81070\_f\_at H81070 2006 RNA helicase-related protein 39.64 down 0.00002<BR> rc\_H87765\_at H87765 2017 KIAA0626 gene product 3.94 down 0.00123<BR> H93246\_s\_at H93246 203 EST 4.14 down 0.00058<BR> rc\_H93381\_at H93381 2036 EST 8.62 down 0.01271<BR> rc\_H99727\_at H99727 2080 adipose differentiation-related protein; adipophilin 3.91 down 0.00325<BR> HG1428-HT1428\_s\_at HG1428-HT1428 hemoglobin, beta 8.98 down 0.02071<BR> HG2379-HT3996\_s\_at HG2379-HT3996 serine hydroxymethyltransferase 1 (soluble) 3.81 down 0.01837<BR> HG2730-HT2827\_s\_at HG2730-HT2827 fibrinogen, A alpha polypeptide 3.84 down 0.00795 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> HG2730-HT2828\_s\_at HG2730-HT2828 fibrinogen, A alpha polypeptide 3.62 down 0.01013<BR> HG2841-HT2968\_s\_at HG2841-HT2968 albumin 4.62 down 0.00552<BR> HG4533-HT4938\_at HG4533-HT4938 protease inhibitor 4 (kallistatin) 3.35 down 0.01605<BR> J02843\_at J02843 2088 cytochrome P450, subfamily IIE (ethanol-inducible) 6.18 down 0.01308<BR> solute carrier family 2 (facilitated glucose transporter),<BR> J03810\_at J03810 2099 member 2 3.6 down 0.02376<BR> J03910\_rna1\_at J03910 2101 EST 18.13 down 0.00119<BR> J04093\_s\_at J04093 2106 UDP glycosyltransferase 1 3.28 down 0.02286<BR> cytochrome P450, subfamily IIIA (naphthalene oxidase),<BR> J0449\_at J0449 2110 polypeptide 3 5.07 down 0.01733<BR> J05158\_at J05158 2117 carboxypeptidase N, polypeptide 2, 83kD 3.37 down 0.01156<BR> J05428\_at J05428 2120 UDPglycosyltransferase 2 family, polypeptide B7 4.86 down 0.03414<BR> coagulation factor IX (plasma thromboplastin component,<BR> K02402\_at K02402 2125 Christmas disease, hemophilia B) 6.64 down 0.04082<BR> K02766\_at K02766 2126 complement component 9 5.03 down 0.0433<BR> cytochrome P450, subfamily IIA (phenobarbital-inducible),<BR> K03192\_f\_at K03192 2127 polypeptide 6 14.19 down 0.0307<BR>

cytochrome P450, subfamily IIA (phenobarbital-inducible),<BR> K03192\_f\_at K03192 2127 polypeptide 6 8.02 down 0.03483<BR> low density lipoprotein receptor (familial<BR> L00352\_at L00352 2131 hypercholesterolemia) 3.3 down 0.03487<BR> cytochrome P450, subfamily I (aromatic compound-<BR> L00389\_f\_at L00389 2132 inducible), polypeptide 2 3.87 down 0.00844<BR> L04751\_at L04751 2138 cytochrome P450, subfamily IVA, polypeptide 11 8.13 down 0.02065<BR> L05144\_at L05144 2139 phosphoenolpyruvate carboxykinase 1 (soluble) 4 down 0.021<BR> fatty-acid-Coenzyme A ligase, long-chain 1,fatty-acid-<BR> L09229\_s\_at L09229 2150 Coenzyme A ligase, long-chain 2 4.5 down 0.01347<BR> L11931\_at L11931 2159 serine hydroxymethyltransferase 1 (soluble) 3.74 down 0.0056<BR> L12760\_s\_at L12760 2162 phosphoenolpyruvate carboxykinase 1 (soluble) 6.06 down 0.01005<BR> cytochrome P450, subfamily IIC (mephenytoin 4-<BR> L16883\_s\_at L16883 2166 hydroxylase), polypeptide 9 5.85 down 0.04368 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank SeqID Known Gene Name Fold Change Direction Pvalue<BR> solute carrier family 10 (sodium/bile acid cotransporter<BR> L21893\_at L21893 2176 family), member 1 5.23 down 0.03367<BR> L27050\_at L27050 2186 apolipoprotein F 4.18 down 0.04901<BR> L32140\_at L32140 2192 afamin 5.39 down 0.02767<BR> M10942\_at M10942 2233 mealllothionein 1E (functional) 4.05 down 0.01412<BR> M10943\_at M10943 2234 metallothionein 1F (functional) 6.23 down 0.00007<BR> M13143\_at M13143 2249 kallikrein B plasma, (Fletcher factor) 1 3.04 down 0.008<BR> M14777-s\_at M14777 2263 glutathione S-transferase A2,glutathione S-transferase A3 13.23 down 0.03224<BR> M16594\_at M16594 2272 glutathione S-transferase A2 5.42 down 0.03813<BR> M16750\_s\_at M16750 2273 pim-1 oncogene 3.07 down 0.02391<BR> M16974-s\_at M16974 2277 complemen component 8, alpha polypeptide 10.85 down 0.02313<BR> m25079\_s\_at M25079 2305 hemoglobin, beta 4.31 down 0.01567<BR> M26393\_s\_at M26393 2309acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain 4.3 down 0.02294<BR> M29873\_s\_at M29873 2318 cytochrome P450, subfamily IIB (phenobarbital-inducible) 17.92 down 0.01469<BR> M29874\_s\_at M29874 2319 cytochrome P450, subfamily IIB (phenobarbital-inducible) 8.13 down 0.01604<BR> M30185\_at M30185 2321 cholesteryl ester transfer protein, plasma 3.82 down 0.00131<BR> M30185\_at M30185 2321 cholesteryl ester transfer protein, plasma 3.31 down 0.00109<BR> cytochrome P450, subfamily I (aromatic compound-<BR> M31667\_f\_at M31667 2331 inducible), polypeptide 2 4.47 down 0.01116<BR> cytochrome P450, subfamily IIA (phenobarbital-inducible),<BR> M33317\_f\_at M33317 2338 polypeptide 7 11.47 down 0.02611<BR> M34276\_at M34276 2341 plaswminogen 3.08 down 0.02754<BR> M57731\_s\_at M57731 2359 GRO2 oncogene 3.16 down 0.02204<BR> cytochrome P450, subfamily IIC (mephenytoin -4<BR> M61854-s\_at M61854 2370 hydroxylase) 3.45 down 0.02949<BR> M63967\_at M63967 2378 aldehydr dehydrogenase 5 3.88 down 0.00274<BR> M68840\_at M68840 2388 monoamine oxidase A 3.1 down 0.01953 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq I Known Gene Name Fold Change Direction Pvalue<BR> M68895\_rna1\_at M68895 2390 alcohol dehydrogenase 6 (class V) 3.21 down 0.02095<BR> M72885\_rna1-s\_at M72885 2393 putative lymphocyte G0/G1 switch gene 3.34 down 0.02943<BR> M76665\_at M76665 2398 hydroxysteroid (11-beta) dehydrogenase 1 6.06 down 0.01317<BR> M81349\_at M81349 2405 serum amyloid A4, constitutive 10.97 down 0.01946<BR> M83652\_s\_at M83652 2408 properidin P factor, complement 6 down 0.00002<BR> M83772\_at M83772 2409 flavin containing monooxygenase 3 5.14 down 0.02023<BR> insulin-like growth factor binding protein, acid labile<BR> M86826\_at M86826 2413 subunit 3.75 down 0.01157<BR> M93405\_at M93405 2424 methylmalonate-semialdehyde dehydrogenase 3.09 down 0.03285<BR> M94065-s\_at M94065 2425 dihydroorotate dehydrogenase 7.87 down 0.0011<BR> M94065\_at M94065 2425 dihydroorotate dehydrogenase 3.61 down 0.00229<BR> M95585\_s\_at M95585 2430 hepatic leukemia factor 3.36 down 0.00492<BR> transducin-like enhancer of split 4, homlg of Drosophila<BR> M99439\_at M99439 2438 E(sp1) 4.82 down 0.00121<BR> rc\_N22404\_at N22404 2450 EST 3.44 down 0.02267<BR> rc\_N22938\_s\_at N22938 2453 serum amyloid A4, constitive 4.91 down 0.01918<BR> rc\_N29353\_at N29353 2477 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) 3.44 down 0.01212<BR> rc\_N29764\_at N29764 2482 EST 4.48 down 0.013<BR>

rc\_N31741\_at N31741 2489 serine hydroxymethyltransferase 1 (soluble) 5.66 down 0.00212<BR>  
rc\_N34804\_at N34804 2497 DKFZP434J214 protein 3.97 down 0.0175<BR> rc\_N39163\_at N39163  
2509 metallothionein 1L 4.3 down 0.03917<BR> rc\_N39201\_at N39201 2510 protease inhibitor 4  
(kallistatin) 4.79 down 0.02015<BR> rc\_N49902\_at N49902 2540 EST 3.02 down 0.00951<BR>  
rc\_N51117\_at N51117 2544 EST 8.17 down 0.00105<BR> rc\_N51773\_at N51773 2549 EST 6.92  
down 0.01839<BR> LIM protein (similar to rat protein kinase C-binding<BR> rc\_N52771\_at N52771  
2552 enigma) 3.670 down 0.01102<BR> rc\_N52322\_at N52322 2553 EST 4.58 down 0.02077<BR>  
rc\_N54053\_at N54053 2561 secreted phosphoprotein 2, 24kD 12.87 down 0.01821<BR>  
rc\_N54417\_s\_at N54417 2567 fibrinogen, A alpha polypeptide 6.47 down 0.00733 Table 7A. Up  
regulated in hepatocellular carcinoma versus normal sample set 2<BR> Affy ID Genbank Seq ID Known  
Gene Name Fold Change Direction Pvalue<BR> rc\_N54429\_at N54429 2568 EST 6.85 down  
0.03334<BR> rc\_N54950\_s\_at N54950 2573 ketohexokinase (fructokinase) 6.47 down 0.0223<BR>  
N57464\_at N57464 2576 CCAAT/enhancer binding protein (C/EBP), delta 4.87 down 0.00111<BR>  
rc\_N57934\_s\_at N57934 2577 formiminotransferase cyclodeaminase 3.28 down 0.01555<BR>  
rc\_N58009\_at N58009 2578 formiminotransferase cyclodeaminase 8.52 down 0.01808<BR>  
rc\_N59550\_at N59550 2588 EST 4.78 down 0.02924<BR> rc\_N63391\_at N63391 2600 EST 3.87  
down 0.02935<BR> rc\_N63845\_at N63845 2605 phytanoyl-CoA hydroxylase (Refsum disease) 6.82  
down 0.00369<BR> enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A<BR> rc\_N64036\_s\_at  
N64036 2607 dehydrogenase 6.12 down 0.00476<BR> rc\_N65959\_at N65959 2612 EST 3.38 down  
0.00785<BR> rc\_N66066\_at N66066 2613 EST 4.33 down 0.0184<BR> rc\_N67105\_at N67105 2624  
EST 4.69 down 0.00194<BR> rc\_N68596\_s\_at N68596 2636 betaine-homocysteine methyltransferase  
10.46 down 0.01971<BR> rc\_N70358\_s\_at N70358 2657 growth hormone receptor 8.47 down  
0.00816<BR> slute carrier family 10 (sodium/bile acid cotransporter<BR> rc\_N70966\_s\_at N70966  
2663 family), member 1 10.8 down 0.02894<BR> rc\_N73543\_at N73543 2675 EST 4.64 down  
0.03981<BR> rc\_N74025\_at N74025 2685 deiodinase, iodothyronine, type I 8.18 down 0.01363<BR>  
N77326\_at N77326 29696 EST 4.08 down 0.00768<BR> rc\_N80129\_i\_at N80129 2703  
metallothionein 1L 26.87 down 0.00999<BR> rc\_N80129\_f\_at N80129 2703 metallothionein 1L 11.48  
down 0.00167<BR> rc\_N90584\_at N90584 2714 EST 3.36 down 0.01561<BR> N91087\_at N91087  
2717 EST 3.66 down 0.00725<BR> N99542\_at N99542 2747 orosomucoid 1 3.53 down 0.00607<BR>  
rc\_R01023\_s\_at R01023 2752 glucokinase (hexokinase 4) regulatory protein 4.56 down 0.04036<BR>  
rc\_R08564\_at R08564 2780 plasminogen-like 8.77 down 0.01284<BR> rc\_R09053\_at R09053 2783  
EST 3.45 down 0.03074<BR> rc\_R12472\_at R12472 2789 EST 12.09 down 0.02379<BR>  
rc\_R22905\_at R22905 2801 EST 4.31 down 0.01744<BR> rc\_R40395\_s\_at R40395 2841 lecithin-  
cholesterol acyltransferase 12.85 down 0.01334 Table 7A. Up regulated in hepatocellular carcinoma  
versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change  
Direction Pvalue<BR> rc\_R40492\_at R40492 2842 EST 6.4 down 0.00527<BR> rc\_R40899\_f\_at  
R40899 2844 glycine receptor, beta 4.84 down 0.02369<BR> rc\_R43799\_at R43799 2851 EST 3.93  
down 0.005<BR> rc\_R49602\_at R49602 2885 EST 16.17 down 0.00279<BR> rc\_R59722\_at R59722  
2916 EST 6.24 down 0.02361<BR> rc\_R65593\_s\_at R65593 2935 kynurenine 3-monooxygenase  
(kynurenine 3-hydroxylase) 6.6 down 0.01982<BR> rc\_R66002\_at R66002 2936 EST 4.33 down  
0.00789<BR> R69417\_at R69417 2942 EST 6.43 down 0.00778<BR> rc\_R73816\_at R73816 2961  
EST 7.05 down 0.01287<BR> R77628\_at R77628 2966 insulin induced gene 1 5.51 down 0.0404<BR>  
R79750\_at R79750 2971 EST 4.89 down 0.00695<BR> R80048\_at R80048 2972 EST 3.61 down  
0.01209<BR> rc\_R89811\_s\_at R89811 2980 HGF activator 13.29 down 0.00148<BR> rc\_R92475\_s\_at  
R92475 2987 flevin containing monooxygenase 3 6.46 down 0.02269<BR> rc\_R93714\_at R93714  
2992 fetuin B 4.65 down 0.03704<BR> R93776\_s\_at R93776 2993 EST 5.55 down 0.00084<BR>  
rc\_R94674\_s\_at R94674 2996 EST 4.58 down 0.0047<BR> cytochrome P450, subfamily VIIIB (sterol  
12-alpha-<BR> rc\_R97419\_at R97419 3004 hydroxylase), polypeptide 1 19.3 down 0.00807<BR>  
R98073\_at R98073 3009 EST 8.37 down 0.01436<BR> rc\_R99591\_at R99591 3016 CD5 antigen-like  
(scavenger receptor cysteine rich family) 7.41 down 0.00043<BR> aldo-keto reductase family 1,  
member C4 (chlordencome<BR> reduclase; 3-alpha hydroxysteroid dehydrogenase, type I;<BR>

S68287\_at S68287 3025 dihydrodiol dehydrogenase 4) 5.04 down 0.02895<BR> S70004\_at S70004  
 3029 glycogen synthase 2 (liver) 5.13 down 0.00183<BR> S77356\_at S77356 3034 EST 3.56 down  
 0.03874<BR> rc\_T10264\_s\_at T10264 3051 EST 3.26 down 0.01718<BR> rc\_T16484\_s\_at T16484  
 3071 EST 4.78 down 0.00009<BR> rc\_T40936\_at T40936 3118 EST 4.62 down 0.02844 Table 7A. Up  
 regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID  
 Known Gene Name Fold Change Direction Pvalue<BR> rc\_T40995\_f\_at T40995 3119 alcohol  
 dehydrogenase 3 (class I), gamma polypeptide 3.42 down 0.00957<BR> rc\_T41047\_s\_at T41047 3120  
 EST 3.08 down 0.00553<BR> rc\_T41232\_at T41232 3122 EST 3.14 down 0.02012<BR>  
 rc\_T47778\_s\_at T47778 3127 fibrinogen, A alpha polypeptide 3.33 down 0.00637<BR>  
 rc\_T48075\_f\_at T48075 3130 hemoglobin, alpha 1 35.75 down 0.00471<BR> rc\_T48278\_at T48278  
 3132 EST 24.1 down 0.00595<BR> rc\_T51150\_at T51150 3137 EST 8.65 down 0.00553<BR> solute  
 carrier family 22 (extraneuronal monoamine<BR> rc\_T51617\_at T51617 3138 transporter), member 3  
 6.16 down 0.04198<BR> rc\_T52813\_s\_at T52813 3142 putative lymphocyte G0/G1 switch gene 5.4  
 down 0.02021<BR> rc\_T56281\_f\_at T56281 3151 RNA helicase-related protein 14.64 down  
 0.00027<BR> T57140\_s\_at T57140 3152 paraoxonase 3 8.47 down 0.01048<BR> rc\_T58756\_at  
 T58756 3156 EST 16.61 down 0<BR> rc\_T61256\_s\_at T61256 3162 ketohexokinase (fructokinase)  
 3.56 down 0.04957<BR> rc\_T61649\_f\_at T61649 3165 superoxide dismutase 2, mitochondrial 4.08  
 down 0.0389<BR> ficolin (collagen/fibrinogen domain-containing) 3 (Hakata<BR> rc\_T63364\_at  
 T63364 3170 antigen) 6.27 down 0.00455<BR> rc\_T64575\_s\_at T64575 3172 EST 3.16 down  
 0.01855<BR> rc\_T67931\_at T67931 3184 fibrinogen, B beta polypeptide 17.25 down 0.00128<BR>  
 T68510\_at T68510 3187 EST 3.19 down 0.01504<BR> rc\_T68711\_at T68711 3188 EST 35.98 down  
 0.0003<BR> rc\_T68873\_f\_at T68873 3190 metallothionein 1L 13.68 down 0.00593<BR>  
 carboxylesterase 1 (monocyte/macrophage serine<BR> rc\_T68878\_f\_at T68878 3191 esterase 1) 4.18  
 down 0.02474<BR> rc\_T69305\_at T69305 3197 EST 15.87 down 0.02258<BR> rc\_T72502\_at T72502  
 3208 EST 4.74 down 0.00404<BR> rc\_T72906\_at T72906 3210 EST 4.91 down 0.00512<BR>  
 rc\_T74542\_s\_at T74542 3215 UDP glycosyltransferase 2 family, polypeptide B10 7.19 down  
 0.011<BR> rc\_T74608\_at T74608 3216 hydroxyacid oxidase (glycolate oxidase) 1 6.1 down  
 0.00249<BR> rc\_T78433\_s\_at T78433 3220 glycogen synthase 2 (liver) 5.74 down 0.00949<BR>  
 T83397\_at T83397 3233 phytanoyl-CoA hydroxylase (Refsum disease) 8.03 down 0.02173 Table 7A.  
 Up regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID  
 Known Gene Name Fold Change Direction Pvalue<BR> rc\_T87174\_at T87174 3240 EST 3.46 down  
 0.00026<BR> T95813\_f\_at T95813 3262 KIAA1051 protein 20.36 down 0.01361<BR>  
 rc\_T98199\_i\_at T98199 3267 EST 4.05 down 0.00753<BR> rc\_T98676\_at T98676 3269 EST 11.15  
 down 0.0323<BR> U02388\_at U02388 3278 cytochrome P450, subfamily IVF, polypeptide 2 4.4 down  
 0.00761<BR> U06641\_s\_at U06641 3287 UDP glycosyltransferase 2 family, polypeptide B15 6.37  
 down 0.01594<BR> U08006\_s\_at U08006 3290 complement component 8, alpha polypeptide 3.96  
 down 0.04272<BR> U08021\_at U08021 3291 nicotinamide N-methyltransferase 3.63 down  
 0.03726<BR> U20530\_at U20530 3322 secreted phosphoprotein 2, 24kD 5.31 down 0.01119<BR>  
 U21931\_at U21931 3326 fructose-bisphosphatase 1 3.17 down 0.0143<BR> cytochrome P450,  
 subfamily IIA (phenobarbital-inducible),<BR> U22029\_f\_at U22029 3327 polypeptide 7 11.85 down  
 0.03538<BR> solute carrier family 6 (neurotransmitter transporter,<BR> U27699\_at U27699 3340  
 betaine/GABA), member 12 3.65 down 0.00381<BR> U50196\_at U50196 3377 adenosine kinase 3.03  
 down 0.00975<BR> U50929\_at U50929 3380 betaine-homocysteine methyltransferase 8.04 down  
 0.0188<BR> U51010\_s\_at U51010 3381 nicotinamide N-methyltransferase 4.69 down 0.03099<BR>  
 U56814\_at U56814 3393 deoxyribonuclease I-like 3 17.69 down 0.00007<BR> U56814\_at U56814  
 3393 deoxyribonuclease I-like 3 5.75 down 0.00152<BR> U65932\_at U65932 3405 extracellular matrix  
 protein 1 3.18 down 0.00575<BR> U95090\_at U95090 3464 nephrosis 1, congenital, Finnish type  
 (nephrin) 4.63 down 0.01595<BR> W07723\_at W07723 3471 EST 3.51 down 0.00026<BR>  
 W26996\_at W26996 3484 EST 4.46 down 0.00734<BR> W28414\_at W28414 3490 EST 4.06 down  
 0.00083<BR> W28798\_at W28798 3492 phosphodiesterase 6A, cGMP-specific, rod, alpha 3.33 down  
 0.00222<BR> W28944\_at W28944 3494 EST 6.9 down 0.01014<BR> rc\_W44745\_at W44745 3520

EST 3.87 down 0.01051<BR> rc\_W45560\_at W45560 3525 EST 3.48 down 0.0179<BR> W55903\_at W55903 3546 adipose differentiation-related protein; adipophilin 5.64 down 0.00014<BR> rc\_W63728\_at W63728 3565 EST 3.86 down 0.00288<BR> rc\_W67147\_at W67147 3568 deleted in liver cancer 1 4.37 down 0.00069 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_W72044\_at W72044 3580 insulin induced gene 1 3.1 down 0.03445<BR> oxidative 3 alpha hydroxysteroid dehydrogenase; retinol<BR> rc\_W72382\_at W72382 3584 dehydrogenase 9.89 down 0.03091<BR> rc\_W73601\_at W73601 3592 EST 3.45 down 0.01382<BR> rc\_W73818\_at W73818 3593 EST 3.47 down 0.00927<BR> rc\_W81552\_at W81552 3615 EST 12.97 down 0.00244<BR> rc\_W86075\_at W86075 3624 EST 6.04 down 0.01486<BR> rc\_W86600\_at W86600 3628 EST 3.67 down 0.04208<BR> rc\_W87532\_at W87532 3634 putative glycine-N-acyltransferase 5.5 down 0.00739<BR> rc\_W87781\_at W87781 3636 EST 4.02 down 0.00284<BR> rc\_W88946\_at W88946 3639 putative glycine-N-acyltransferase 25.28 down 0.00221<BR> rc\_W95041\_at W95041 3662 EST 4.22 down 0.01005<BR> X02176\_s\_at X02176 3672 complement component 9 3.84 down 0.01793<BR> X06562\_at X06562 3686 growth hormone receptor 4.8 down 0.00507<BR> X06985\_at X06985 3689 heme oxygenase (decycling) 1 3.34 down 0.00045<BR> X13277\_at X13277 3698 D-amino-acid oxidase 3.22 down 0.01753<BR> cytochrome P450, subfamily IIA (phenobarbital-inducible),<BR> X13930\_f\_at X13930 3700 polypeptide 6 8.1 down 0.0219<BR> acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-<BR> X14813\_at X14813 3705 oxoacyl-Coenzyme A thiolase0 3.53 down 0.00059<BR> X16260\_s\_at X16260 3710 inter-alpha (globulin) inhibitor, H1 polypeptide 3.76 down 0.00291<BR> X16349\_s\_at X16349 3712 sex hormone-binding globulin 6.61 down 0.00008<BR> X54380\_at X54380 3730 pregnancy-zone protein 7.71 down 0.00069<BR> X56411\_ma1\_at X56411 3737 alcohol dehydrogenase 4 (class II), pi polypeptide 9.87 down 0.01416<BR> X58022\_at X58022 3747 corticotropin releasing hormone-binding protein 4.09 down 0.00076<BR> X63359\_at X63359 3759 UDP glycosyltransferase 2 family, polypeptide B10 4.26 down 0.01725<BR> X64177\_f\_at X64177 3763 metallothionein 1H 3.26 down 0.03928<BR> X67491\_f\_at X67491 3776 glutamate dehydrogenase 1 4.06 down 0.00273<BR> X72177\_ma1\_at X72177 3790 complement component 6 4.25 down 0.01598<BR> X76717\_at X76717 3797 metallothionein 1L 5.64 down 0.00215<BR> X90579\_s\_at X90579 3819 EST 4.26 down 0.04759 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> X95190\_at X95190 3832 acyl-Coenzyme A oxidase 2, branched chain 6.22 down 0.00162<BR> X97324\_at X97324 3839 adipose differentiation-related protein; adipophilin 3.72 down 0.00202<BR> Y00317\_at Y00317 3845 UDP glycosyltransferase 2 family, polypeptide B4 4.63 down 0.02986<BR> Z20777\_at Z20777 3866 EST 15.73 down 0.00147<BR> aldo-keto reductase family 1, member D1 (delta 4-3-<BR> Z28339\_at Z28339 3875 ketosteroid-5-beta-reductase) 8.03 down 0.00853<BR> lipase A, lysosomal acid, cholesterol esterase (Wolman<BR> Z31690\_s\_at Z31690 3881 disease) 3.29 down 0.00161<BR> rc\_Z40259\_s\_at Z40259 3919 EST 4.47 down 0.00093<BR> rc\_Z40305\_at Z40305 3920 EST 4.09 down 0.00096<BR> rc\_Z40902\_at Z40902 3926 SEC14 (S. cerevisiae)-like 2 4.97 down 0.04627<BR> rc\_Z41042\_at Z41042 3928 EST 3.37 down 0.00703<BR> Z48475\_at Z48475 3943 glucokinase (hexokinase 4) regulatory protein 4.6 down 0.01693<BR> small inducible cytokine subfamily A (Cys-Cys), member<BR> Z49269\_at Z49269 3945 14 7.24 down 0.01047<BR> Z69923\_at Z69923 3948 HGF activator 3.95 down 0.00012<BR> Z80345\_ma1\_s\_at Z80345 3951 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain 3.21 down 0.04734<BR> Z84721\_cds2\_at Z84721 3953 hemoglobin, zeta 7.39 down 0.01921 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA001504\_f\_at AA001504 2 EST 4.44 up 0.03077<BR> rc\_AA005262\_at AA005262 13 EST 3.09 up 0.0064<BR> KIAA1080 protein; Golgi-associated, gamma-adaptin ear<BR> rc\_AA007507\_at AA007507 18 containing, ARF-binding protein 2 5.23 up 0.00159<BR> rc\_AA010065\_s\_at AA010065 22 CDC28 protein kinase 2 3.71 up 0.00432<BR> rc\_AA011209\_s\_at AA011209 30 melanoma-associated antigen recognised by T 6.45 up 0.00088<BR> rc\_AA011679\_at AA011679 32 EST 3.08 up



0.03649<BR> rc\_AA018346\_at AA018346 38 EST 3.69 up 0.04582<BR> rc\_AA021549\_at AA021549 42 EST 3.17 up 0.00158<BR> rc\_AA022623\_at AA022623 44 EST 3.27 up 0.01556<BR> rc\_AA024658\_at AA024658 47 ribosomal protein S19 7.55 up 0.00592<BR> rc\_AA024776\_at AA024776 48 EST 3.44 up 0.00334<BR> rc\_AA025166\_s\_at AA025166 50 fusion, derived from t (12;16) malignant liposarcoma 3.17 up 0.00009<BR> rc\_AA026356\_at AA026356 57 EST 5.04 up 0.02483<BR> rc\_AA027833\_i\_at AA027833 59 EST 5.02 up 0.01123<BR> rc\_AA029288\_at AA029288 65 EST 3.36 up 0.04908<BR> rc\_AA031814\_at AA031814 70 KIAA0958 protein 3.07 up 0.00681<BR> rc\_AA037058\_s\_at AA037058 84 laminin, gamma 1 (formerly LAMB2) 4.11 up 0.02264<BR> rc\_AA037433\_at AA037433 86 EST 4.9 up 0.0194<BR> rc\_AA037766\_at AA037766 87 EST 3.63 up 0.0328<BR> rc\_AA040465\_at AA040465 95 EST 3.63 up 0.01806<BR> AA043111\_s\_at AA043111 97 EST 6.36 up 0.0005<BR> rc\_AA043959\_at AA043959 101 tropomyosin 4 4.37 up 0.01641<BR> rc\_AA045365\_at AA045365 106 EST 3.17 up 0.0149<BR> rc\_AA046103\_at AA046103 109 EST 3.75 up 0.02893<BR> rc\_AA046410\_s\_at AA046410 110 EST 3.18 up 0.00797<BR> rc\_AA046745\_at AA046745 113 Wolf-Hirschhorn syndrome candidate 1 3.33 up 0.00648<BR> rc\_AA047379\_s\_at AA047379 119 karyopherin (importin) beta 1 3.15 up 0.01572<BR> rc\_AA047704\_at AA047704 120 EST 3.2 up 0.0029<BR> rc\_AA052941\_at AA052941 121 EST 3.36 up 0.00088<BR> rc\_AA053662\_f\_at AA053662 129 EST 3.3 up 0.00558 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA053680\_at AA053680 130 high-mobility group protein 2-like 1 4.07 up 0.03144<BR> rc\_AA055892\_at AA055892 134 EST 3.02 up 0.04984<BR> rc\_AA055896\_at AA055896 135 collagen, type V, alpha 1 10.87 up 0.00907<BR> rc\_AA070206\_at AA070206 155 EST 3.15 up 0.03914<BR> rc\_AA070485\_at AA070485 156 interleukin 13 receptor, alpha 1 3.19 up 0.03465<BR> rc\_AA070827\_at AA070827 157 EST 4.37 up 0.02617<BR> AA071387\_at AA071387 158 jumping translocation breakpoint 3.31 up 0.0001<BR> rc\_AA074162\_s\_at AA074162 159 superkiller viralicidic activity 2 (S. cerevisiae homolog)- 3.23 up 0.00642<BR> rc\_AA076138\_at AA076138 167 H2A histone family, member Y 3.75 up 0.01442<BR> rc\_AA086071\_at AA086071 184 chromosome-associated polypeptide c 3.77 up 0.01993<BR> kangai 1 (suppression of tumorigenicity 6, prostate;<BR> CD82 antigen (R2 leukocyte antigen, antigen detected<BR> rc\_AA086232\_f\_at AA086232 186 by monoclonal and antibody IA4)) 4.52 up 0.00452<BR> rc\_AA086412\_at AA086412 187 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 3.13 up 0.00327<BR> AA089997\_at AA089997 189 EST 4.9 up 0.0241<BR> AA091752\_at AA091752 193 purine-rich element binding protein B 3.25 up 0.01419<BR> AA092129\_f\_at AA092129 194 EST 5.67 up 0.00011<BR> AA092290\_f\_at AA092290 195 EST 3.25 up 0.01616<BR> AA094752\_at AA094752 203 hypothetical 43.2 Kd protein 3.44 up 0.04445<BR> rc\_AA099404\_s\_at AA099404 208 EST 20.22 up 0<BR> rc\_AA101272\_at AA101272 215 EST 3.83 up 0.0386<BR> rc\_AA102489\_at AA102489 219 EST 5.28 up 0.02122<BR> rc\_AA102837\_f\_at AA102837 221 EST 4.13 up 0.0067<BR> rc\_AA112679\_at AA112679 224 EST 4.19 up 0.00572<BR> rc\_AA115562\_at AA115562 229 EST 3.35 up 0.00283<BR> rc\_AA115735\_s\_at AA115735 230 EST 4.8 up 0.02671<BR> rc\_AA116036\_at AA116036 233 chromosome 20 open reading frame 1 3.41 up 0.00089<BR> rc\_AA122386\_at AA122386 239 collagen, type v, alpha 2 3.44 up 0.02566<BR> rc\_AA125808\_at AA125808 240 EST 3.04 up 0.02112<BR> rc\_AA127444\_at AA127444 252 EST 3.87 up 0.01751<BR> rc\_AA127741\_at AA127741 256 EST 4.49 up 0.0463 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA128407\_at AA128407 259 EST 3.33 up 0.02298<BR> rc\_AA129757\_at AA129757 264 EST 3.75 up 0.0166<BR> rc\_AA131220\_at AA131220 267 EST 3.18 up 0.00974<BR> rc\_AA132032\_s\_at AA132032 271 trinucleotide repeat containing 1 3.84 up 0.01136<BR> rc\_AA132514\_at AA132514 272 EST 3.2 up 0.00876<BR> rc\_AA133527\_at AA133527 281 EST 5.23 up 0.00037<BR> rc\_AA133666\_s\_at AA133666 283 cysteine-rich protein 2 5.35 up 0.00433<BR> rc\_AA134052\_s\_at AA134052 285 Rab geranylgeranyltransferase, alpha subunit 5.47 up 0.00982<BR> rc\_AA135153\_at AA135153 291 EST 5.58 up 0.00327<BR> rc\_AA135871\_at AA135871 294 EST 3.56 up 0.01718<BR> rc\_AA136269\_at AA136269 298 EST 7.5 up 0.00014<BR>



rc\_AA136474\_at AA136474 301 Meis (mouse) homolog 2 3.15 up 0.02837<BR> rc\_AA136547\_at AA136547 302 EST 4.19 up 0.00098<BR> rc\_AA136864\_at AA136864 304 zinc finger protein homologous to Zfp-36 in mouse 3.31 up 0.00346<BR> rc\_AA142857\_at AA142857 307 EST 9.48 up 0.00376<BR> rc\_AA142858\_at AA142858 308 EST 4.07 up 0.0022<BR> rc\_AA146849\_s\_at AA146849 313 target of myb1 (chicken) homolog 4.72 up 0.00326<BR> rc\_AA148885\_at AA148885 320 minichromosome maintenance deficient (S. cerevisiae) 4 6.59 up 0.00112<BR> rc\_AA148977\_at AA148977 322 EST 9.3 up 0.00002<BR> rc\_AA149889\_at AA149889 326 neighbor of A-kinase anchoring protein 95 8.55 up 0.00224<BR> rc\_AA151435\_at AA151435 336 EST 4.52 up 0.01134<BR> ATP synthase, H<sup>+</sup> transporting, mitochondrial F0<BR> rc\_AA156187\_at AA156187 339 complex, subunit b, isoform 1 9.38 up 0.02007<BR> rc\_AA156460\_at AA156460 343 EST 4.39 up 0.01223<BR> rc\_AA159025\_at AA159025 353 EST 6.58 up 0.01946<BR> rc\_AA160775\_s\_at AA160775 355 BCL2-antagonist of cell death 3.8 up 0.01145<BR> 3-prime-phosphoadenosine 5-prime-phosphosulfate<BR> rc\_AA165526\_at AA165526 360 synthase 1 3.68 up 0.00021<BR> rc\_AA167708\_at AA167708 363 EST 3.19 up 0.01871<BR> rc\_AA171760\_at AA171760 367 EST 4.39 up 0.04582<BR> rc\_AA173430\_at AA173430 371 EST 3.74 up 0.01159 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> AA173505\_at AA173505 372 EST 3 up 0.01736<BR> AA173597\_at AA173597 373 EST 3.37 up 0.03622<BR> rc\_AA173755\_at AA173755 374 EST 6.73 up 0.00666<BR> rc\_AA179787\_at AA179787 380 polyglutamine binding protein 1 4.71 up 0.00725<BR> rc\_AA179845\_at AA179845 381 EST 3.55 up 0.02484<BR> rc\_AA181580\_s\_at AA181580 383 karyopherin (importin) beta 1 3.01 up 0.0125<BR> rc\_AA181705\_f\_at AA181705 385 EST 5.9 up 0.00023<BR> rc\_AA182001\_r\_at AA182001 386 EST 3.78 up 0.04446<BR> AA187579\_at AA187579 390 MCT-1 protein 3.4 up 0.02455<BR> rc\_AA188378\_i\_at AA188378 392 EST 4.88 up 0.01653<BR> rc\_AA194730\_at AA194730 410 EST 4.57 up 0.00801<BR> rc\_AA194998\_at AA194998 413 purinergic receptor (family A group 5) 3.06 up 0.04752<BR> rc\_AA195067\_i\_at AA195067 414 GTPase activating protein-like 3.24 up 0.00606<BR> rc\_AA204927\_at AA204927 425 tropomyosin 1 (alpha) 6.11 up 0.0014<BR> rc\_AA207103\_at AA207103 429 EST 3.36 up 0.00131<BR> rc\_AA211483\_at AA211483 435 EST 4.11 up 0.0365<BR> AA215299\_s\_at AA215299 439 U6 snRNA-associated Sm-like protein LSm7 4.81 up 0.00119<BR> rc\_AA215379\_at AA215379 440 EST 4.44 up 0.01675<BR> rc\_AA218663\_at AA218663 444 acid-inducible phosphoprotein 4.34 up 0.00161<BR> rc\_AA226932\_at AA226932 453 DKFZP564F0923 protein 5.25 up 0.00612<BR> rc\_AA227145\_at AA227145 454 EST 3.4 up 0.03422<BR> rc\_AA227541\_at AA227541 457 ns1-binding protein 3.6 up 0.02801<BR> AA232837\_at AA232837 465 EST 8.85 up 0.0048<BR> rc\_AA233897\_at AA233897 476 EST 3.8 up 0.02145<BR> rc\_AA234096\_at AA234096 479 EST 5.75 up 0.01169<BR> rc\_AA235289\_at AA235289 495 RAP2A, member of RAS oncogene family 4.31 up 0.00135<BR> AA235448\_s\_at AA235448 497 EST 5.62 up 0.00077<BR> rc\_AA235853\_at AA235853 503 CGI-96 protein 3.16 up 0.00744<BR> rc\_AA235868\_at AA235868 504 nuclear transcription factor Y, beta 3.49 up 0.01897<BR> 3-prime-phosphoadenosine 5-prime-phosphosulfate<BR> rc\_AA236150\_at AA236150 507 synthase 1 3.46 up 0.0008 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> AA236412\_at AA236412 511 EST 3.1 up 0.04463<BR> rc\_AA236532\_s\_at AA236532 513 EST 3.04 up 0.03747<BR> rc\_AA236672\_at AA236672 515 EST 4.37 up 0.00385<BR> rc\_AA236904\_at AA236904 518 EST 3.07 up 0.01503<BR> rc\_AA242757\_at AA242757 522 EST 3.27 up 0.00286<BR> rc\_AA243133\_at AA243133 525 serine/threonine kinase 15 7.03 up 0.00005<BR> rc\_AA243173\_at AA243173 526 EST 3.49 up 0.0401<BR> AA249819\_s\_at AA249819 535 EST 5.22 up 0.00049<BR> rc\_AA251230\_at AA251230 540 EST 3.25 up 0.01417<BR> rc\_AA251299\_s\_at AA251299 541 KIAA0014 gene product 4.74 up 0.0252<BR> rc\_AA251428\_at AA251428 542 DKFZP58612223 protein 3.15 up 0.01223<BR> rc\_AA251766\_at AA251766 543 EST 3.06 up 0.0098<BR> rc\_AA251769\_at AA251769 544 EST 4.45 up 0.01431<BR> rc\_AA251792\_at AA251792 546 fatty-acid-Coenzyme A ligase, long-chain 4 7.44 up 0.00285<BR> rc\_AA251909\_at AA251909

549 EST 3.59 up 0.01129<BR> rc\_AA252060\_at AA252060 550 EST 4.88 up 0.00169<BR>  
 rc\_AA252355\_at AA252355 553 EST 3.02 up 0.00715<BR> rc\_AA252524\_at AA252524 555 EST  
 3.17 up 0.00686<BR> chaperonin containing TCP1, subunit 6A (zeta 1), homeo<BR>  
 rc\_AA252627\_s\_at AA252627 556 box B5 4.28 up 0.00363<BR> rc\_AA253011\_f\_at AA253011 558  
 KIAA0713 protein 3.15 up 0.00035<BR> rc\_AA255486\_at AA255486 568 EST 3.72 up 0.00154<BR>  
 rc\_AA256131\_at AA256131 574 glycerophosphatidylinositol anchor attachment 1 3.16 up 0.00011<BR>  
 rc\_AA256268\_at AA256268 576 EST 3.13 up 0.03874<BR> rc\_AA256524\_at AA256524 580 AD022  
 protein 3.06 up 0.00626<BR> rc\_AA256606\_at AA256606 581 EST 3.92 up 0.03087<BR>  
 rc\_AA256688\_s\_at AA256688 584 EST 4.23 up 0.03094<BR> rc\_AA258131\_at AA258131 587  
 putative GTP-binding protein similar to RAY/RAB1C 6.23 up 0.00931<BR> rc\_AA258182\_at  
 AA258182 589 EST 3.55 up 0.01198<BR> rc\_AA258387\_at AA258387 594 EST 3.15 up  
 0.02028<BR> rc\_AA258421\_at AA258421 595 hypothetical protein 6.5 up 0.00559 Table 7B. Down  
 regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID  
 Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA258614\_s\_at AA258614 599 EST 3.94  
 up 0.0048<BR> rc\_AA262477\_at AA262477 608 ribonuclease HI, large subunit 4.57 up 0.00724<BR>  
 rc\_AA262957\_at AA262957 612 EST 3.76 up 0.00157<BR> ATP synthase, H<sup>+</sup> transporting,  
 mitochondrial F0<BR> AA263032\_s\_at AA263032 614 complex, subunit b, isoform 1 6.73 up  
 0.04478<BR> rc\_AA278768\_f\_at AA278768 617 EST 3.77 up 0.03239<BR> rc\_AA278817\_at  
 AA278817 618 EST 3.5 up 0.01159<BR> rc\_AA279418\_at AA279418 626 EST 3.23 up 0.02054<BR>  
 rc\_AA280734\_i\_at AA280734 639 KIAA0618 gene product 6.83 up 0.001<BR> rc\_AA280840\_at  
 AA280840 641 casein kinase 1, gamma 2 4.51 up 0.0186<BR> rc\_AA281599\_at AA281599 647 EST  
 4.87 up 0.00248<BR> rc\_AA282247\_at AA282247 657 EST 5.88 up 0.01112<BR> rc\_AA282343\_at  
 AA282343 658 purine-rich element binding protein B 5.78 up 0.00128<BR> rc\_AA282571\_at  
 AA282571 662 FSHD region gene 1 3.16 up 0.01355<BR> rc\_AA283182\_at AA283182 668 EST 6.78  
 up 0.01784<BR> rc\_AA283832\_at AA283832 672 EST 4.77 up 0.00156<BR> rc\_AA284565\_f\_at  
 AA284565 675 EST 3.27 up 0.0362<BR> rc\_AA284720\_at AA284720 676 EST 3.03 up 0.00252<BR>  
 rc\_AA284945\_at AA284945 680 EST 6.25 up 0.0002<BR> rc\_AA285132\_at AA285132 682 apoptotic  
 protease activating factor 3.1 up 0.00844<BR> rc\_AA286911\_at AA286911 684 EST 3.36 up  
 0.00037<BR> rc\_AA291137\_at AA291137 694 EST 3.67 up 0.03243<BR> rc\_AA291139\_at  
 AA291139 695 EST 6.22 up 0.03491<BR> rc\_AA291168\_at AA291168 696 EST 4.93 up  
 0.01633<BR> rc\_AA291644\_at AA291644 701 EST 3.28 up 0.00033<BR> rc\_AA291659\_at  
 AA291659 702 EST 4.15 up 0.00019<BR> AA291786\_s\_at AA291786 704 FE65-LIKE 2 4.15 up  
 0.00362<BR> rc\_AA292765\_at AA292765 712 ZW10 interactor 7.24 up 0.00498<BR>  
 rc\_AA292788\_s\_at AA292788 714 EST 3.65 up 0.01765<BR> rc\_AA293420\_s\_at AA293420 717  
 EST 4.05 up 0.01189<BR> rc\_AA293589\_s\_at AA293589 719 zinc finger protein 3.02 up 0.01809  
 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID  
 genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> AA293868\_s\_at AA293868  
 721 EST 3.04 up 0.0054<BR> AA296994\_s\_at AA296994 724 seven transmembrane domain protein  
 3.16 up 0.0076<BR> AA313213\_at AA313213 732 flotillin 1 3.59 up 0.00878<BR> AA320369\_s\_at  
 AA320369 735 chromosome 19 open reading frame 3 3.88 up 0.00452<BR> rc\_AA321833\_at  
 AA321833 736 EST 3.16 up 0.00523<BR> rc\_AA335191\_f\_at AA335191 741 creatine kinase, brain  
 6.47 up 0.01462<BR> rc\_AA338760\_at AA338760 744 EST 3.96 up 0.01307<BR> rc\_AA365708\_s\_at  
 AA365708 764 microfibrillar-associated protein 1 3.01 up 0.02372<BR> AA365742\_s\_at AA365742  
 765 tetraspan NET-6 protein 4.12 up 0.00255<BR> rc\_AA370163\_at AA370163 766 EST 3.41 up  
 0.00134<BR> AA384184\_s\_at AA384184 774 DKFZP586B0519 protein 3.42 up 0.01222<BR>  
 AA393139\_at AA393139 775 geminin 7.44 up 0.008888<BR> rc\_AA394258\_s\_at AA394258 779 RD  
 RNA-binding protein 7.27 up 0.00054<BR> rc\_AA398141\_at AA398141 788 EST 3.3 up 0.0021<BR>  
 rc\_AA398205\_at AA398205 789 EST 4.22 up 0.00059<BR> rc\_AA398563\_at AA398563 797 EST  
 3.14 up 0.01895<BR> rc\_AA398908\_at AA398908 801 EST 20.72 up 0.00114<BR>  
 rc\_AA398926\_f\_at AA398926 802 EST 8.25 up 0.00066<BR> rc\_AA399251\_at AA399251 804 EST  
 4.3 up 0.01578<BR> rc\_AA399264\_at AA399264 805 EST 3.51 up 0.00327<BR> rc\_AA400184\_at

AA400184 809 KIAA0907 protein 4.11 up 0.01123<BR> AA400643\_s\_at AA400643 817 GAS2-related on chromosome 22 4.04 up 0.03751<BR> rc\_AA400896\_at AA400896 822 EST 3.54 up 0.00889<BR> rc\_AA401965\_at AA401965 833 tumor suppressor deleted in oral cancer-related 1 7.58 up 0.00089<BR> rc\_AA402272\_at AA402272 837 EST 3.73 up 0.02336<BR> rc\_AA402968\_at AA402968 844 EST 3.68 up 0.00123<BR> O-linked N-acetylglucosamine (GlcNAc) transferase<BR> (UDP-N-acetylglucosamine:polypeptide-N-<BR> rc\_AA40560\_at AA40560 853 acetylglucosaminyl transferase) 3.73 up 0.0143<BR> rc\_AA405098\_at AA405098 855 EST 6.09 up 0.01224<BR> rc\_Aa405505\_at AA405505 860 RNA helicase family 4.05 up 0.007474 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA405544\_f\_at AA405544 861 EST 3.09 up 0.04146<BR> rc\_AA405791\_at AA405791 864 EST 11.79 up 0.00587<BR> rc\_AA406216\_at AA406216 871 EST 3.4 up 0.00529<BR> rc\_AA406384\_at AA406384 875 KIAA0670 protein/acinus 3.23 up 0.00486<BR> rc\_AA410469\_at AA410469 883 EST 5.45 up 0.00068<BR> rc\_AA410962\_s\_at AA410962 887 peroxisome proliferative activated receptor, delta 4.91 up 0.0044<BR> rc\_AA412301\_at AA412301 899 eST 3.42 up 0.0129<BR> rc\_AA412720\_at AA412720 905 EST 3.06 up 0.02153<BR> rc\_AA416970\_at AA416970 912 Mad4 homology 5.3 up 0.00418<BR> rc\_AA416973\_at AA416973 913 EST 4.29 up 0.00155<BR> rc\_AA417030\_at AA417030 914 EST 7.35 up 0.00555<BR> rc\_AA417884\_at AA417884 919 cyclin-dependent kinase inhibitor 2C (p18,inhibitin 3.42 up 0.02997<BR> AA421213\_at AA21213 931 Lsm3 protein 3.34 up 0.00198<BR> rc\_AA421562\_at AA421562 934 anterior gradient 2 (Xenopus laevis) homolog 5.02 up 0.02818<BR> rc\_AA421951\_at AA421951 936 EST 6.69 up 0.00013<BR> rc\_AA423827\_f\_at AA423827 941 chromosome 22 open reading frame 3 4.39 up 0.00345<BR> rc\_AA423841\_f\_at AA423841 942 EST 3.71 up 0.01481<BR> rc\_AA424029\_at AA424029 943 EST 4.54 up 0.02721<BR> rc\_AA424487\_at AA424487 945 EST 4.68 up 0.0013<BR> rc\_AA424881\_at AA424881 949 EST 3.39 up 0.03546<BR> eukaryotic translation initiation factor 2B, subunit 2 (beta,<BR> rc\_AA425544\_s\_at AA425544 955 39kD) 3.05 up 0.0346<BR> rc\_AA425852\_at AA425852 958 EST 3.98 up 0.02796<BR> rc\_AA425852\_i\_at AA425852 958 EST 3.82 up 0.0395<BR> rc\_AA426291\_at AA426291 961 EST 3.03 up 0.00365<BR> rc\_AA426374\_f\_at AA426374 964 tubulin, alpha 2 3.25 up 0.04346<BR> rc\_AA426447\_at AA426447 965 EST 3.01 up 0.02414<BR> rc\_AA426521\_at AA426521 967 Sjogren's syndrome nuclear autoantigen 1 3.33 up 0.01163<BR> rc\_AA427734\_at AA427734 977 cholinergic receptor, nicotinic, epsilon polypeptide 3.08 up 0.04796<BR> AA428172\_f\_at AA428172 986 Notch (Drosophila) homolog 3 9.63 up 0.00195 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene name Fold Change Direction Pvalue<BR> rc\_AA428204\_at AA428204 987 subunit 6 (77kD) 3.08 up 0.00313<BR> rc\_AA429470\_at AA429470 996 EST 3.2 up 0.0153<BR> rc\_AA429472\_at AA429472 997 DKFZP434P106 protein 8.78 up 0.00063<BR> rc\_AA429539\_f\_at AA429539 999 EST 4.3 up 0.01035<BR> rc\_AA429572\_at AA429572 1000 ribosomal protein S6 3.31 up 0.02144<BR> rc\_AA429825\_at AA429825 1003 DKFZP566B023 protein 3.11 up 0.01857<BR> rc\_AA430032\_at AA430032 1009 pituitary tumor-transforming 1 10.67 up 0.00052<BR> rc\_AA43048\_at AA43048 1012 KIAA0160 protein 4.32 up 0.00279<BR> rc\_AA430154\_at AA430154 1014 EST 3.09 up 0.04401<BR> rc\_AA430474\_at AA430474 1015 EST 4.69 up 0.00007<BR> rc\_AA430675\_at AA430675 1019 Fanconi anemia, complementation group G 3.16 up 0.01007<BR> rc\_AA431571\_at AA431571 1024 EST 4.62 up 0.0174<BR> rc\_AA431719\_at AA431719 1025 EST 3.19 up 0.00294<BR> rc\_AA433947\_at AA433947 1034 EST 3.09 up 0.00253<BR> rc\_AA434418\_at AA434418 1036 KIAA1115 protein 6.75 up 0.0032<BR> rc\_AA435662\_f\_at AA435662 1039 EST 3.27 up 0.0433<BR> rc\_AA435665\_at AA435665 1040 EST 3.94 up 0.00274<BR> rc\_AA435681\_s\_at AA435681 1041 EST 3.07 up 0.01166<BR> rc\_AA435748\_at AA435748 1044 EST 5.01 up 0.01812<BR> rc\_aa435769\_s\_at AA435769 1046 EST 3.06 up 0.00615<BR> rc\_AA442054\_s\_at AA442054 1067 phospholipase C, gamma 1 (formerly subtype 148) 4.94 up 0.04102<BR> rc\_AA442155\_at AA442155 1068 transforming acidic coiled-coil containing protein 3 3.35 up 0.00344<BR> rc\_AA442400\_at AA442400 1071 hepatitis B virus x-

interacting protein (9.6kD) 3.02 up 0.04037<BR> rc\_AA442763\_at AA442763 1072 cyclin B2 3.49 up 0.04176<BR> rc\_AA443271\_at AA443271 1073 KIAA0546 protein 3.44 up 0.00324<BR> rc\_AA443316\_s\_at AA443316 1075 v-Ha-ras Harvey rat sarcoma viral oncogene homolog 3.4 up 0.00133<BR> rc\_AA443602\_at AA443602 1078 EST 5.71 up 0.00736<BR> rc\_AA443802\_at AA443802 1081 EST 4.07 up 0.01546<BR> rc\_AA446242\_at AA446242 1087 EST 6.3 up 0.00169<BR> rc\_AA446570\_at AA446570 1089 EST 3.12 up 0.02228 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA446581\_at AA446581 1090 DKFZP564P0462 protein 4.04 up 0.00479<BR> rc\_AA446970\_at AA446970 1098 EST 3.09 up 0.01627<BR> rc\_AA447574\_at AA447574 1102 EST 4.12 up 0.00779<BR> rc\_AA448252\_at AA448252 1114 EST 3 up 0.00256<BR> rc\_aa449073\_s\_at AA449073 1117 EST 5.61 up 0.01214<BR> rc\_aa449431\_s\_at AA449431 1124 translation initiation factor IF2 3.76 up 0.00571<BR> rc\_AA449828\_at AA449828 1130 EST 3.35 up 0.01609<BR> rc\_AA450247\_at AA450247 1133 EST 3.13 up 0.00531<BR> hepatocellular carcinoma associated protein; breast<BR> rc\_AA451680\_at AA451680 1136 cancer associated gene 1 3.85 up 0.0018<BR> rc\_AA451877\_at AA451877 1138 EST 4.6 up 0.04045<BR> AA451992\_at AA451992 1140 HSPC039 protein 3.33 up 0.01696<BR> rc\_AA452167\_at AA452167 1142 EST 3.29 up 0.03337<BR> AA452724\_at AA452724 1149 programmed cell death 5 7.7 up 0.00085<BR> rc\_AA453628\_at AA453628 1154 EST 3.17 up 0.00849<BR> rc\_AA453656\_at AA453656 1155 EST 3.02 up 0.00958<BR> rc\_AA453783\_s\_at AA453783 1158 EST 4.07 up 0.00786<BR> rc\_AA454597\_s\_at AA454597 1166 EST 4.23 up 0.00917<BR> rc\_AA454830\_at AA454830 1170 DKFZP586M2123 protein 6.48 up 0.00555<BR> AA454908\_s\_at AA454908 1171 KIAA0144 gene product 6.39 up 0.01835<BR> rc\_AA455239\_at AA455239 1174 chromosome-associated polypeptide C 5.78 up 0.00003<BR> rc\_AA456415\_at AA456415 1192 KIAA0537 gene product 3.32 up 0.00155<BR> rc\_AA456583\_s\_at AA456583 1193 PL6 protein 3.37 up 0.00139<BR> rc\_AA456646\_at AA456646 1196 EST 3.34 up 0.0309<BR> rc\_AA456852\_at AA456852 1199 supressor of white apricot homolog 2 3.66 up 0.00614<BR> rc\_AA458878\_s\_at AA458878 1204 EST 5.49 up 0.00977<BR> rc\_AA458890\_at AA458890 1206 EST 3.27 up 0.00079<BR> rc\_AA459254\_at AA459254 1211 EST 6.22 up 0.00001<BR> rc\_AA459542\_s\_at AA459542 1218 regulatory factor X-associated ankyrin-containing protein 3.4 up 0.00841<BR> rc\_AA460665\_at AA460665 1230 EST 4.01 up 0.01866<BR> rc\_aa460909\_s\_at AA460909 1232 EST 5.02 up 0.01354 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA461063\_at AA461063 1235 EST 4.3 up 0.00074<BR> AA461282\_s\_at AA461282 1237 dihydropyrimidinase-like 2 3.42 up 0.02014<BR> rc\_AA461476\_at AA461476 1243 EST 3.72 up 0.00744<BR> rc\_AA463254\_s\_at AA463254 1247 histone deacetylase 3 4.01 up 0.01856<BR> rc\_AA463934\_at AA463934 1253 splicing factor 3b, subunit 4, 49kD 3.15 up 0.00592<BR> rc\_AA464043\_s\_at AA464043 1255 EST 3.99 up 0.00056<BR> rc\_AA464251\_s\_at AA464251 1257 EST 3.45 up 0.02229<BR> rc\_AA464414\_i\_at AA464414 1258 EST 4.08 up 0.02299<BR> rc\_AA464423\_at AA464423 1259 EST 3.06 up 0.01416<BR> rc\_aa464722\_s\_at AA464722 1263 KFZP566C243 protein 3.51 up 0.00101<BR> rc\_AA464963\_at AA464963 1265 EST 4.77 up 0.00086<BR> AA465000\_s\_at AA465000 1266 EST 3.86 up 0.00431<BR> rc\_AA465093\_at AA465093 1267 TIA1 cytotoxic granule-associated RNA-binding protein 3.3 up 0.01314<BR> rc\_AA465218\_at AA465218 1268 DKFP586M1523 protein 3.17 up 0.00357<BR> rc\_AA465342\_at AA465342 1271 EST 3.21 up 0.01378<BR> rc\_AA470156\_at AA470156 1276 EST 4.99 up 0.0206<BR> AA471384\_at AA471384 1278 divalent cation tolerant protein CUTA 3.44 up 0.01161<BR> rc\_AA476473\_at AA476473 1285 EST 3 up 0.01324<BR> rc\_AA476754\_s\_at AA476754 1287 EST 3.18 up 0.01696<BR> rc\_AA476944\_at AA476944 1288 EST 3.29 up 0.00189<BR> rc\_AA477316\_at AA477316 1290 calcumenin 3.05 up 0.00608<BR> rc\_AA477549\_s\_at AA477549 1291 T-cell, immune regulator 1 4.84 up 0.04906<BR> rc\_AA478017\_at AA478017 1295 zyxin 4.25 up 0.01223<BR> rc\_AA478300\_at AA478300 1298 CD39-like 2 3.75 up 0.00152<BR> rc\_AA478415\_at AA478415 1299 EST 3.14 up 0.0483<BR> rc\_AA478422\_at AA478422 1301 unc-51 (C. elegans)-like kinase 1 3.83 up 0.00116<BR>

rc\_AA478615\_s\_at AA478615 1305 H1 histone family, member X 3.09 up 0.0499<BR> disabled (Drosophila) homolog 2 (mitogen-responsive<BR> rc\_AA478971\_s\_at AA478971 1306 phosphoprotein) 3.25 up 0.02698<BR> rc\_AA479096\_at AA479096 1308 EST 3.32 up 0.00118<BR> rc\_AA479139\_s\_at AA479139 1310 acid phosphatase 1, soluble 3.42 up 0.01853 Table 7B. Down Regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA47988\_at AA479881 1317 EST 3.34 up 0.3289<BR> rc\_AA481060\_at AA481060 1326 EST 3.08 up 0.00029<BR> rc\_AA481420\_at AA481420 1327 EST 3.08 up 0.0206<BR> rc\_AA482104\_s\_at AA482104 1332 no-metastatic cells 3, protein expressed in 4.78 up 0.00135<BR> rc\_AA482224\_f\_at AA482224 1334 putative type II membrane protein 4.47 up 0.0001<BR> AA482319\_f\_at AA482319 1335 putative type II membrane protein 4.9 up 0.00028<BR> AA482319\_i\_at AA482319 1335 putative type II membrane protein 3.13 up 0.00071<BR> rc\_AA485060\_at AA485060 1339 EST 3.83 up 0.03172<BR> rc\_AA485084\_s\_at AA485084 1340 EST 3.31 up 0.01232<BR> rc\_AA485431\_s\_at AA485431 1345 EST 3.81 up 0.00441<BR> rc\_AA485697\_at AA485697 1346 EST 3.53 up 0.03566<BR> rc\_AA487218\_at AA487218 1355 EST 4.43 up 0.03198<BR> rc\_AA487856\_at AA487856 1359 KIAA0676 protein 3.59 up 0.1408<BR> rc\_AA48807\_at AA488074 1360 cell division cycle 42 (GTP-binding protein, 25kD) 3.74 up 0.01887<BR> rc\_AA88432\_at AA48432 1361 phosphoserine phosphatase 4.2 up 0.00128<BR> rc\_AA88872\_s\_at AA488872 1363 EST 3.35 up 0.03191<BR> rc\_AA488892\_at AA488892 1364 EST 4.14 up 0.04766<BR> rc\_AA489091\_at AA489091 1368 EST 3.58 up 0.0002<BR> rc\_AA489707\_at AA489707 1371 EST 3.5 up 0.03208<BR> rc\_AA489712\_at AA489712 1372 EST 4.69 up 0.00587<BR> rc\_AA490212\_at AA490212 1375 H2A histone family, member Y 3.52 up 0.02202<BR> solute carrier family 2 (facilitated glucose transporter),<BR> AA491188\_at AA491188 1387 member 3 5.04 up 0.02291<BR> rc\_AA491295\_at AA491295 1390 calcium/calmodulin-dependent protein kinase kinase 2, 3.71 up 0.0103<BR> AA495857\_at AA495857 1394 EST 3.21 up 0.02243<BR> rc\_AA496715\_f\_at AA496715 1400 spectrin SH3 domain binding protein 1 3.44 up 0.00069<BR> v-erb-b2 avian erythroblastic leukemia viral oncogene<BR> rc\_AA496981\_at AA496981 1404 homolog 3 5.82 up 0.00521<BR> rc\_AA497018\_at AA497018 1406 adenylate cyclase 1 (brain) 4.81 up 0.00352<BR> AA054413\_at AA504413 1413 EST 3.31 up 0.00036<BR> rc\_AA504512\_s\_at AA504512 1415 KIAA0943 protein 5.72 up 0.00384 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> solute carrier family 2 (facilitated glucose transporter),<BR> rc\_AA505133\_at AA505133 1417 member 3 12.21 up 0.00169<BR> rc\_AA505141\_at AA505141 1418 EST 3.08 up 0.02327<BR> rc\_AA521149\_at AA521149 1420 EST 3.33 up 0.00211<BR> rc\_AA598405\_at AA598405 1424 membrane interacting protein of RGS16 3.87 up 0.00649<BR> rc\_AA598447\_at AA598447 1428 exportin, tRNA (nuclear export receptor for tRNAs) 3.5 up 0.01201<BR> rc\_AA598589\_at AA598589 1431 EST 3.24 up 0.00432<BR> SWI/SNF related, matrix associated, actin dependent<BR> rc\_AA598648\_s\_at AA598648 1432 regulator of chromatin, subfamily a, member 4 3.46 up 0.00293<BR> rc\_AA598712\_at AA598712 1436 EST 3.45 up 0.00005<BR> rc\_AA598749\_at AA598749 1438 EST 3.01 up 0.03714<BR> heterogeneous nuclear ribonucleoprotein U (scaffold<BR> rc\_AA598829\_s\_at AA598829 1439 attachment factor A) 3.04 up 0.00967<BR> rc\_AA598831\_f\_at AA598831 1440 EST 3.41 up 0.00452<BR> rc\_AA599469\_at AA599469 1450 EST 3.07 up 0.04154<BR> rc\_AA599808\_at AA599808 1455 EST 3.09 up 0.00726<BR> rc\_AA599850\_at AA599850 1457 EST 3.55 up 0.03215<BR> rc\_AA600153\_at AA60153 1460 DEK oncogene (DNA binding) 3.71 up 0.02967<BR> rc\_AA608668\_at AA608668 1465 erythrocyte membrane protein band 4.1-like 2 3.33 up 0.02014<BR> rc\_AA608897\_at AA608897 1473 EST 5.05 up 0.01782<BR> rc\_AA609008\_at AA609008 1475 EST 4.04 up 0.00002<BR> rc\_AA609080\_at AA609080 1478 EST 3.71 up 0.0306<BR> rc\_AA610073\_at AA610073 1497 EST 3.25 up 0.00859<BR> rc\_AA610089\_at AA610089 1498 U4/U6-associated RNA splicing factor 4.07 up 0.00361<BR> rc\_AA610116\_i\_at AA610116 1499 tetraspan NET-6 protein 16.35 up 0.00249<BR> rc\_AA620461\_at AA620461 1501 EST 3.45 up 0.01146<BR> rc\_AA620553\_s\_at AA620553 1504 flap structure-specific endonuclease 1 7.56 up 0.00101<BR> rc\_AA620761\_at AA620761 1507 EST 3.3 up



0.00285<BR> rc\_AA620779\_at AA620779 1508 golgin-67 3.35 up 0.00297<BR> rc\_AA620881\_at AA620881 1510 trinucleotide repeat containing 3 9.49 up 0.00062<BR> rc\_AA621146\_at AA621146 1514 MUF1 protein 3.15 up 0.02116 table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_AA621242\_s\_at AA621242 1518 hypothetical protein,peptidylprolyl isomerase B 4.59 up 0.00081<BR> rc\_AA621367\_at AA621367 1523 EST 3.1 up 0.00066<BR> rc\_AA621409\_at AA621409 1524 putative type II membrane protein 3.5 up 0.00462<BR> rc\_AA621530\_at AA621530 1526 EST 3.26 up 0.00298<BR> rc\_AA621535\_at AA621535 1527 FE65-LIKE 2 3.37 up 0.0167<BR> rc\_AA621752\_at AA621752 1529 26S proteasome-associated pad1 homolog 3.13 up 0.01571<BR> AB002373\_at AB002373 1538 KIAA0375 gene product 4.41 up 0.00795<BR> AF003521\_at AF003521 1545 jagged 2 3.58 up 0.00299<BR> AF004022\_at AF004022 1546 serine/threonine kinase 12 3.29 up 0.00841<BR> C00358\_at C00358 1552 nucleolar protein 3 (apoptosis repressor with CARD 3.45 up 0.00985<BR> C01721\_at C01721 1558 phospholipase C, beta 3, neighbor pseudogene 5.89 up 0.0383<BR> C01766\_s\_at C01766 1559 EST 8.18 up 0.00505<BR> rc\_C14051\_f\_at C14051 1565 phosphorprotein enriched in astrocytes 15 4.79 up 0.00548<BR> rc\_C14098\_f\_at C14098 1566 EST 4.62 up 0.01654<BR> rc\_C14756\_f\_at C14756 1570 MLN51 protein 3.75 up 0.0226<BR> rc\_C14835\_f\_at C14835 1571 EST 3.35 up 0.0316<BR> D00596\_at D00596 1590 thymidylate synthetase 5.58 up 0.0098<BR> D13370\_at D13370 1603 APEx nuclease (multifunctional DNA repair enzyme) 3.07 up 0.00857<BR> general transcription factor IIIC, polypeptide 2 (beta<BR> D13636\_at D13636 1606 subunit, 110kD) 3.12 up 0.00022<BR> D13640\_at D13640 1608 KIAA0015 gene product 3.55 up 0.00347<BR> D14657\_at D14657 1615 KIAA0101 gene product 3.84 up 0.02048<BR> rc\_D20899\_at D20899 1626 EST 3.13 up 0.02128<BR> minichromosome maintenance deficient (S. cerevisiae) 2<BR> D21063\_at D21063 1628 (mitotin) 3.25 up 0.03558<BR> D26129\_at D26129 1635 ribonuclease, RNase A family, 1 (pancreatic) 6.9 up 0.00008<BR> D28589\_at D28589 1637 EST 3.38 up 0.01144<BR> D30946\_at D30946 1638 kinesin family member 3B 3.43 up 0.01458<BR> D31094\_at D31094 1639 G8 protein 9.37 up 0.0048<BR> D31294\_at D31294 1643 EST 3.3 up 0.004<BR> D31417\_at D31417 1645 secreted protein of unknown function 3.69 up 0.0004 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> D38073\_at D38073 1651 minichromosome maintenance deficient (S. cerevisiae) 3 4.1 up 0.01195<BR> D38305\_at D38305 1652 transducer of ERBB2, 1 3.22 up 0.0215<BR> D42040\_s\_at D42040 1657 female sterile homeotic-related gene 1 (mouse homolog) 4.02 up 0.00389<BR> rc\_D51072\_s\_at D51072 1674 biliverdin reductase A 3.34 up 0.0254<BR> rc\_D51276\_f\_at D51276 1678 leukemia-associated phosphoprotein p18 (stathmin) 9.42 up 0.00015<BR> D55716\_at D55716 1686 minichromosome maintenance deficient (S. cerevisiae) 7 5.48 up 0.00003<BR> rc\_D57317\_at D57317 1688 activated RNA polymerase II transcription cofactor 4 3.17 up 0.00464<BR> rc\_D59355\_s\_at D59355 1696 cytoskeleton-associated protein 1 6.05 up 0.0015<BR> rc\_D59553\_f\_at D59553 1697 golgin-67 5.95 up 0.00169<BR> rc\_D59570\_f\_at D59570 1699 EST 4.34 up 0.00487<BR> rc\_D60811\_s\_at D60811 1704 EST 4.34 up 0.00217<BR> D63478\_at D63478 1711 KIAA0144 gene product 3.89 up 0.00253<BR> D63486\_at D63486 1712 KIAA0152 gene product 3.56 up 0.00063<BR> rc\_D80420\_at D80420 1732 ubiquinol-cytochrome c reductase hinge protein 3.86 up 0.00412<BR> rc\_D80710\_f\_at D80710 1734 integral type I protein 3.17 up 0.04549<BR> rc\_D80917\_f\_at D80917 1736 KIAA0670 protein/acinus 3.09 up 0.00168<BR> rc\_D80946\_f\_at D80946 1737 SFRS protein kinase 1 3.07 up 0.00986<BR> D81608\_at D81608 1740 polymerase (RNA) II (DNA directed) polypeptide K 3.52 up 0.00437<BR> D82226\_s\_at D82226 1742 proteasome (prosome, macropain) 26S subunit, 4.35 up 0.00184<BR> D82277\_s\_at D82277 1743 LDL induced EC protein 3.33 up 0.00355<BR> D82558\_at D82558 1746 novel centrosomal protein RanBPM 4.67 up 0.00458<BR> trinucleotide repeat containing 11 (THR-associated<BR> D83783\_at D83783 1748 protein, 230 kDa subunit) 4.16 up 0.00055<BR> D84557\_at D84557 1749 minichromosome maintenance deficient (mis5, S. 3.97 up 0.0017<BR> D86957\_at D86957 1754 KIAA0202 protein 3.08 up 0.02949<BR> D86977\_at D86977 1757 KIAA0224 gene product 3.03 up 0.00053<BR> rc\_F01538\_s\_at F01538 1771 RAP1, GTPase activating protein 1 4.88

up 0.00292<BR> rc\_F01568\_at F01568 1772 EST 4.13 up 0.00084<BR> rc\_F01831\_at F01831 1773 EST 5.95 up 0.00532<BR> rc\_F02254\_s\_at F02254 1777 Fas-activated serine/threonine kinase 5.1 up 0.00329<BR> rc\_F02807\_at F02807 1781 KIAA0838 protein 5.67 up 0.02064 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_F02863\_at F02863 1782 EST 3.05 up 0.03504<BR> rc\_F04320\_s\_at F04320 1786 replication factor C (activator 1) 4 (37kD) 6.29 up 0.00042<BR> rc\_F04444\_at F04444 1788 EST 4.13 up 0.00944<BR> rc\_F04479\_at F04479 1789 KIAA1067 protein 3.23 up 0.04522<BR> rc\_F08876\_at F08876 1797 EST 9.06 up 0<BR> procollagen-proline, 2-oxoglutarate 4-dioxygenase<BR> rc\_F09788\_at F09788 1808 (proline 4-hydroxylase), alpha polypeptide II 3.67 up 0.01682<BR> rc\_F10199\_f\_at F10199 1813 EST 3.93 up 0.03209<BR> rc\_F10290\_at F10290 1815 EST 3.39 up 0.02392<BR> rc\_F10453\_at F10453 1819 EST 3.64 up 0.01878<BR> rc\_F10741\_at F10741 1822 KIAA0622 protein 3.01 up 0.03079<BR> rc\_F13809\_f\_at F13809 1828 tropomyosin 1 (alpha) 4.4 up 0.01221<BR> rc\_H00540\_at H00540 1829 EST 3.74 up 0.00234<BR> rc\_H05084\_at H05084 1844 EST 5.85 up 0.0059<BR> rc\_H07873\_at H07873 1856 EST 3.53 up 0.0391<BR> rc\_H08863\_at H08863 1859 hypothetical protein 7.18 up 0.02102<BR> rc\_H09241\_s\_at H09241 1861 EST 3.05 up 0.01487<BR> rc\_H09271\_f\_at H09271 1862 EST 4.78 up 0.00072<BR> rc\_H10933\_at H10933 1873 EST 6.18 up 0.00003<BR> rc\_H11320\_s\_at H11320 1875 SUMO-1 activating enzyme subunit 2 3.06 up 0.00167<BR> rc\_H16251\_s\_at H16251 1886 EST 3.3 up 0.03286<BR> rc\_H27188\_f\_at H27188 1908 collagen-binding protein 2 (collagen 2) 5.84 up 0.01826<BR> rc\_H27897\_s\_at H27897 1911 hypothetical protein 3.01 up 0.00174<BR> rc\_H28333\_f\_at H28333 1912 melanoma adhesion molecule 4.94 up 0.00166<BR> rc\_H41529\_at H41529 1926 EST 5.06 up 0.03309<BR> rc\_H46486\_s\_at H46486 1932 nesca protein 4.57 up 0.00749<BR> rc\_H47357\_f\_at H47357 1934 EST 3.65 up 0.03799<BR> rc\_H48459\_s\_at H48459 1937 KIAA0186 gene product 3.1 up 0.02325<BR> rc\_H52937\_at H52937 1944 roundabout (axon guidance receptor, Drosophila) 4.02 up 0.00163<BR> rc\_H56345\_r\_at H56345 1950 EST 3.73 up 0.00853<BR> rc\_H57709\_s\_at H57709 1956 ribosomal protein L31 4.41 up 0.00091 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_H59617\_at H59617 1964 EST 5.81 up 0.0115<BR> rc\_H62474\_f\_at H62474 1970 EST 3.39 up 0.04173<BR> rc\_H64493\_f\_at H64493 1973 immunoglobulin heavy constant gamma 3 (G3m marker) 4.74 up 0.00751<BR> rc\_H65030\_s\_at H65030 1974 acetylhydrolase, plasma) 3.26 up 0.02278<BR> rc\_H65042\_at H65042 1975 EST 3.44 up 0.0006<BR> rc\_H67964\_at H67964 1981 EST 3.06 up 0.02707<BR> rc\_H68794\_at H68794 1984 EST 3.67 up 0.00327<BR> rc\_H70739\_f\_at H70739 1991 EST 4.34 up 0.00106<BR> rc\_H73484\_s\_at H73484 1995 ferritin, heavy polypeptide 1 3.18 up 0.00432<BR> rc\_H78211\_at H78211 2001 EST 7.5 up 0.02674<BR> rc\_H86072\_f\_at H86072 2015 EST 4.49 up 0.01301<BR> rc\_H88674\_s\_at H88674 2021 collagen, type I, alpha 2 4.15 up 0.02664<BR> rc\_H89987\_s\_at H89987 2027 ATP-binding cassette, sub-family C (CFTR/MRP), 3.13 up 0.01194<BR> rc\_H91632\_at H91632 2031 EST 3.5 up 0.03688<BR> rc\_H94471\_at H94471 2042 occludin 6.26 up 0.00379<BR> rc\_H96850\_at H96850 2055 dolichyl-diphosphooligosaccharide-protein 3.03 up 0.00679<BR> rc\_H97012\_at H97012 2058 EST 3.51 up 0.03505<BR> rc\_H97013\_at H97013 2059 ephrin-A4 6.8 up 0.00023<BR> rc\_H97677\_s\_at H97677 2062 EST 4.34 up 0.00753<BR> rc\_H99261\_s\_at H99261 2074 EST 3.33 up 0.00319<BR> rc\_H99364\_at H99364 2075 chloride channel 7 3.03 up 0.01727<BR> rc\_H99473\_s\_at H99473 2077 regulator of nonsense transcripts 1 6.51 up 0.00025<BR> rc\_H99489\_s\_at H99489 2078 quiescin Q6 3.4 up 0.02682<BR> rc\_H99587\_s\_at H99587 2079 EST 4.44 up 0.00532<BR> rc\_H99774\_at H99774 2081 EST 3.51 up 0.00009<BR> rc\_H99877\_at H99877 2083 exportin, tRNA (nuclear export receptor for tRNAs) 3.75 up 0.00302<BR> rc\_H99879\_at H99879 2084 EST 10.81 up 0.001 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> J00231\_f\_at J00231 2087 immunoglobulin heavy constant gamma 3 (G3m marker) 6.23 up 0.00177<BR> J03040\_at J03040 2091 secreted protein, acidic, cysteine-rich (osteonectin) 3.77 up 0.00594<BR> J03464\_s\_at J03464 2094 collagen, type I, alpha 2 10.37 up

0.00979<BR> keratin 10 (epidermolytic hyperkeratosis; keratosis<BR> J04029\_s\_at J04029 2102  
 palmaris et plantaris) 3.02 up 0.00032<BR> J05614\_at J05614 2122 EST 3.73 up 0.03419<BR>  
 L03411\_s\_at L03411 2134 RD RNA-binding protein 4.06 up 0.00467<BR> L04270\_at L04270 2135  
 lymphotoxin beta receptor (TNFR superfamily, member 3.5 up 0.01547<BR> L06797\_s\_at L06797  
 2143 chemokine (C-X-C motif), receptor 4 (fusin) 3.23 up 0.04782<BR> L11669\_at L11669 2157  
 tetracycline transporter-like protein 3.4 up 0.02062<BR> high-mobility group (nonhistone  
 chromosomal) protein<BR> L17131\_rna1\_at L17131 2168 isoforms I and Y 4.45 up 0.03141<BR>  
 TATA box binding protein (TBP)-associated factor, RNA<BR> L25444\_at L25444 2181 polymerase  
 II, E, 70/85kD 3.78 up 0.00011<BR> cyclin-dependent kinase inhibitor 3 (CDK2-associated<BR>  
 L25876\_at L25876 2182 dual specificity phosphatase) 4.43 up 0.00082<BR> L28821\_at L28821 2188  
 mannosidase, alpha, class 2A, member 2 4.63 up 0.00876<BR> L29218\_s\_at L29218 2190 CDC-like  
 kinase 2 6.51 up 0.00019<BR> L29218\_at L29218 2190 CDC-like kinase 2 3.82 up 0.00035<BR>  
 L33930\_s\_at L33930 2198 CD24 antigen (small cell lung carcinoma cluster 4 4.35 up 0.3968<BR>  
 transcription elongation factor B (SIII), polypeptide 1<BR> L34587\_at L34587 2200 (15kD, elongin C)  
 3.12 up 0.00946<BR> L47125\_s\_at L47125 2218 glypican 3 10.69 up 0.04129<BR> L76191\_at  
 L76191 2222 interleukin-1 receptor-associated kinase 1 3.85 up 0.00152<BR> excision repair cross-  
 complementing rodent repair<BR> L76568\_xpt3\_f\_at L76568 2225 deficiency, complementation group  
 4 3.4 up 0.0172<BR> M12125\_at M12125 2241 tropomyosin 2 (beta) 7.13 up 0.0004<BR>  
 M14483\_rna1\_s\_at M14483 2261 prothymosin, alpha (gene sequence 28) 3.36 up 0.00033<BR>  
 M19267\_s\_at M19267 2286 tropomyosin 1 (alpha) 4.3 up 0.00893 Table 7B. Down regulated in  
 hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene  
 Name Fold Change Direction Pvalue<BR> M21259\_at M21259 2293 small nuclear ribonucleoprotein  
 polypeptide E 3.68 up 0.00415<BR> M26576\_cds2\_at M26576 2310 EST 3.48 up 0.00062<BR> AFF-  
 M27830\_5\_at M27830 2314 EST 4.6 up 0.04719<BR> AFF-M27830\_M\_at M27830 2314 EST 3.54 up  
 0.00777<BR> AFF-M27830\_5\_at M27830 2314 EST 3.3 up 0.02453<BR> M31303\_rna1\_at M31303  
 2327 leukemia-associated phosphoprotein p18 (stathmin) 5.86 up 0.00071<BR> M32977\_s\_at M32977  
 2336 vascular endothelial growth factor 3.93 up 0.04917<BR> v-erb-b2 avian erythroblastic leukemia  
 viral oncogene<BR> M34309\_at M34309 2342 homolog 3 3.49 up 0.00191<BR> M35252\_at M35252  
 2343 transmembrane 4 superfamily member 3 4.65 up 0.04128<BR> M37583\_at M37583 2349 H2A  
 histone family, member Z 4.25 up 0.00135<BR> M55210\_at M55210 2353 laminin, gamma 1 (formerly  
 LAMB2) 3.47 up 0.02551<BR> M55998\_s\_at M55998 2356 collagen, type I, alpha 1 3.54 up  
 0.01449<BR> M57710\_at M57710 2357 lecti, galactoside-binding, soluble, 3 (galectin 3) 6.76 up  
 0.00103<BR> M57730\_at M57730 2358 ephrin-A1 3.39 up 0.00199<BR> M60784\_s\_at M60784 2368  
 small nuclear ribonucleoprotein polypeptide A 4.74 up 0.00001<BR> M61916\_at M61916 2372  
 laminin, beta 1 3.18 up 0.01171<BR> M63573\_at M63573 2377 peptidylprolyl isomerase B  
 (cyclophilin B) 3.59 up 0.00916<BR> M68864\_at M68864 2389 ORF 3.95 up 0.00144<BR>  
 M86667\_at M86667 2411 nucleosome assembly protein 1-like 1 3.08 up 0.00473<BR> stress-induced-  
 phosphoprotein 1 (Hsp70/Hsp90-<BR> M86752\_at M86752 2412 organizing protein) 5.15 up  
 0.02881<BR> M87339\_at M87339 2415 replication factor C (activator 1) 4 (37kD) 4.59 up  
 0.00116<BR> M91083\_at M91083 2419 chromosome 11 open reading frame 13 3.19 up 0.00243<BR>  
 membrane component, chromosomal 4, surface marker<BR> M93036\_at M93036 2422 (35kD  
 glycoprotein) 3.07 up 0.04199<BR> M94250\_at M94250 2426 midkine (neurite growth-promoting  
 factor 2) 9.86 up 0.02104<BR> M94345\_at M94345 2427 capping protein (actin filament), gelsolin-like  
 3.59 up 0.04508<BR> M97856\_at M97856 2436 nuclear autoantigenic sperm protein (histone-binding)  
 3.21 up 0.00444<BR> rc\_N21407\_at N21407 2443 EST 3.47 up 0.01037<BR> rc\_N21648\_s\_at  
 N21648 2447 MpV17 transgene, murine homolog, glomerulosclerosis 3.73 up 0.00071 Table 7B. Down  
 regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID  
 Known Gene Name Fold Change Direction Pvalue<BR> rc\_N26904\_at N26904 2469 EST 15.38 up  
 0.00077<BR> rc\_N29484\_at N29484 2478 EST 3.08 up 0.04834<BR> rc\_N29742\_at N29742 2481  
 EST 3.74 up 0.00104<BR> rc\_N31597\_s\_at N31597 2487 DKFZP564G2022 protein 3.17 up  
 0.03017<BR> rc\_N33920\_at N33920 2493 diubiquitin 50.29 up 0<BR> rc\_N34825\_s\_at N34825 2498

DKFZP434P106 protein 3.27 up 0.01334<BR> rc\_N35913\_at N35913 2503 EST 3.48 up 0.0016<BR> rc\_N36432\_at N36432 2507 erythrocyte membrane protein band 4.1-like 2 7.95 up 0.00067<BR> rc\_N29237\_at N29237 2511 EST 3.45 up 0.02481<BR> N42272\_s\_at N42272 2515 EST 3.03 up 0.0017<BR> eukaryotic translation initiation factor 3, subunit 3<BR> rc\_N47956\_at N47956 2524 (gamma, 40kD) 3.76 up 0.00968<BR> rc\_N48790\_at N48790 2532 EST 3.32 up 0.00654<BR> rc\_N51590\_s\_at N51590 2546 EST 3.01 up 0.04345<BR> rc\_N51771\_at N51771 2548 KIAA0652 gene product 3.5 up 0.00028<BR> ADP-ribosyltransferase (NAD<sup>+</sup>; poly (ADP-ribose)<BR> rc\_N51855\_at N51855 2550 polymerase)-like 3 3.39 up 0.00115<BR> rc\_N52168\_at N52168 2551 EST 3.66 up 0.00127<BR> rc\_N53067\_at N53067 25507 DKFZP547E1010 protein 3.1 up 0.00101<BR> rc\_N54067\_at N54067 2562 mitogen-activated protein kinase kinase kinase 4 4.82 up 0.00229<BR> rc\_N54841\_at N54841 2572 EST 5.87 up 0.02752<BR> rc\_N56935\_s\_at N56935 2575 EST 4.04 up 0.00797<BR> rc\_N59536\_at N59536 2586 EST 11.68 up 0.00484<BR> rc\_N62126\_at N62126 2589 EST 6.42 up 0.00109<BR> rc\_N64374\_at N64374 2608 KIAA0537 gene product 3.25 up 0.01652<BR> rc\_N67815\_f\_at N67815 2627 EST 3.84 up 0.00439<BR> rc\_N68018\_at N68018 2631 TBP-associated factor 172 3.84 up 0.00277<BR> rc\_N68241\_at N68241 2634 EST 4.32 up 0.00532<BR> rc\_N69084\_i\_at N69084 2643 EST 3.11 up 0.0094<BR> rc\_N69252\_f\_at N69252 2647 ferritin, light polypeptide 3.69 up 0.04116<BR> rc\_N69263\_at N69263 2648 EST 5.26 up 0.0276 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_N69390\_at N69390 2650 EST 3.99 up 0.00016<BR> rc\_N69879\_s\_at N69879 2651 drebrin 1 3.15 up 0.01659<BR> rc\_N70481\_at N70481 2658 EST 4.13 up 0.0099<BR> rc\_N70678\_s\_at N70678 2660 TAR (HIV) RNA-binding protein 1 3.78 up 0.02858<BR> solute carrier family 11 (proton-coupled divalent metal<BR> rc\_N72116\_s\_at N72116 2668 ion transporters), members 2 5.57 up 0.00709<BR> rc\_N73705\_at N73705 2677 EST 3.75 up 0.01762<BR> rc\_N73762\_f\_at N73762 2678 EST 3.67 up 0.00796<BR> rc\_N73808\_f\_at N73808 2679 EST 6.44 up 0.00352<BR> rc\_N73865\_at N73865 2681 EST 4.43 up 0.00177<BR> rc\_N75541\_at N75541 2692 EST 4.43 up 0.01059<BR> rc\_N80703\_at N80703 2704 EST 5.65 up 0.0001<BR> rc\_N90238\_i\_at N90238 2712 EST 3.13 up 0.02492<BR> rc\_N91773\_at N91773 2719 lysyl oxidase 4.31 up 0.00302<BR> rc\_N92948\_s\_at N92948 2726 nuclear phosphoprotein similar to *S. cerevisiae* PWP1 4.09 up 0.0019<BR> rc\_N93299\_f\_at N93299 2732 nuclear receptor co-repressor 1 6.99 up 0.0371<BR> rc\_N93316\_at N93316 2733 EST 3.16 up 0.01262<BR> rc\_N798\_at N93798 2738 protein tyrosine phosphatase type IVA, member 3 4.91 up 0.00245<BR> rc\_N98464\_s\_at N98464 2744 EST 3.68 up 0.03007<BR> rc\_N98758\_f\_at N98758 2745 EST 3.54 up 0.02609<BR> rc\_N99944\_s\_at N99944 2749 EST 3.46 up 0.00104<BR> rc\_R05316\_s\_at R05316 2760 EST 4.2 up 0.00011<BR> rc\_R06251\_f\_at R06251 2764 tumor protein D52-like 2 4.88 up 0.03097<BR> rc\_R06254\_f\_at R06254 2765 tumor protein D52-like 2 3.53 up 0.04865<BR> rc\_R06400\_at R06400 2768 EST 3.03 up 0.03266<BR> rc\_R06986\_f\_at R06986 2776 peptidylprolyl isomerase B (cyclophilin B) 7.03 up 0.00628<BR> rc\_R07172\_i\_at R07172 2777 EST 5.54 up 0.01322<BR> rc\_R15740\_at R15740 2791 carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 3.36 up 0.00268<BR> rc\_R16144\_at R16144 2794 EST 3.24 up 0.0087<BR> rc\_R20817\_s\_at R20817 2797 ubiquitin-conjugating enzyme E2A (RAD6 homolog) 3.03 up 0.01091<BR> rc\_R22565\_at R22565 2800 EST 3.52 up 0.04352 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_R26744\_at R26744 2804 midline 1 (Opitz/BBB syndrome) 3.8 up 0.00266<BR> myristoylated alanine-rich protein kinase C substrate<BR> rc\_R27016\_s\_at R27016 2806 (MARCKS, 80K-L) 3.53 up 0.03056<BR> rc\_R27296\_f\_at R27296 2807 EST 3.41 up 0.00309<BR> UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase,<BR> rc\_R28636\_at R28636 2809 polypeptide 3 3.06 up 0.03678<BR> rc\_R31607\_at R31607 2813 EST 3.41 up 0.00163<BR> rc\_R33498\_s\_at R33498 2810 EST 3.5 up 0.0336<BR> rc\_R39191\_s\_at R39191 2834 KIAA1020 protein 5.18 up 0.03185<BR> R39390\_at R39390 2837 EST 4.18 up 0.0004<BR> rc\_R39610\_s\_at R39610 2838 calpain, large polypeptide L2 3.13 up 0.01863<BR> rc\_R43952\_at R43952 2853 homeo box B5 3.39 up 0.04829<BR> rc\_R44617\_f\_at R44617 2857 MyoD family inhibitor 6.54 up 0.02505<BR>

rc\_R44793\_at R44793 2859 EST 5.4 up 0.00329<BR> rc\_R44839\_at R44839 2861 i-beta-1,3-N-acetylglucosaminyltransferase 5 up 0.01812<BR> rc\_R454569\_at R45569 2864 DKFZP547E1010 protein 3.96 up 0.00259<BR> rc\_R45994\_f\_at R45994 2867 EST 6.48 up 0.00358<BR> rc\_R46079\_f\_at R46079 2868 EST 3.03 up 0.00755<BR> rc\_R46337\_s\_at R46337 2869 secretory carrier membrane protein 3 3.01 up 0.00374<BR> rc\_R48447\_at R48447 2871 EST 4.76 up 0.00533<BR> rc\_R48473\_f\_at R48473 2872 EST 3.46 up 0.01196<BR> rc\_R48594\_s\_at R48594 2875 EST 6.15 up 0.03831<BR> rc\_R49395\_s\_at R49395 2881 EST 3.31 up 0.00867<BR> rc\_R49476\_at R49476 2883 EST 4.93 up 0.00763<BR> rc\_R49482\_at R49482 2884 EST 3.27 up 0.0161<BR> rc\_R49708\_s\_at R49708 2886 EST 4.56 up 0.03767<BR> rc\_R51908\_s\_at R51908 2892 EST 3.16 up 0.0083<BR> rc\_R52161\_at R52161 2893 EST 3.41 up 0.00053<BR> rc\_R52649\_at R52649 2894 EST 4.69 up 0.00135<BR> rc\_R53109\_f\_at R53109 2899 dimethylarginine dimethylaminohydrolase 2 3.31 up 0.02406<BR> rc\_R54614\_s\_at R54614 2902 EST 3.22 up 0.00334 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_R56095\_s\_at R56095 2906 EST 3.67 up 0.0158<BR> rc\_R60512\_s\_at R60512 2918 KIAA0191 protein 3.08 up 0.00856<BR> rc\_R61374\_at R61374 2921 EST 4.33 up 0.01489<BR> rc\_R61557\_at R61557 2922 KIAA0100 gene product 3.9 up 0.00292<BR> rc\_R62456\_at R62456 2925 EST 3.44 up 0.00285<BR> rc\_R66469\_f\_at R66469 2937 pleckstrin and Sec7 domain protein 3.52 up 0.0272<BR> rc\_R70005\_at R70005 2944 EST 4.98 up 0.00007<BR> rc\_R70253\_at R70253 2945 EST 3.38 up 0.03125<BR> rc\_R70532\_at R70532 2947 EST 3.44 up 0.02186<BR> rc\_R70801\_s\_at R70801 2950 EST 6.06 up 0.00291<BR> rc\_R71395\_at R71395 2952 EST 4.12 up 0.03719<BR> rc\_R72886\_s\_at R72886 2956 KIAA0422 protein 5.5 up 0.00091<BR> rc\_R73569\_s\_at R73569 2960 EST 3.54 up 0.01962<BR> O-linked N-acetylglucosamine (GlcNAc) transferase<BR> (UDP-N-acetylglucosamine:polypeptide-N-<BR> rc\_R76782\_s\_at R76782 2963 acetylglucosaminyl transferase) 3.73 up 0.00094<BR> rc\_R77451\_i\_at R77451 2964 EST 3.67 up 0.00078<BR> rc\_R79246\_f\_at R79246 2969 melanoma adhesion molecule 6.06 up 0.00057<BR> rc\_R91753\_at R91753 2983 EST 3.45 up 0.02391<BR> rc\_R91819\_at R91819 2984 EST 12.81 up 0.00037<BR> rc\_R92449\_s\_at R92449 2985 KIAA0323 protein 4.34 up 0.00104<BR> rc\_R96527\_s\_at R96527 2999 KIAA0253 protein 4.62 up 0.00702<BR> rc\_R96924\_s\_at R96924 3001 EST 7.04 up 0.00012<BR> S67070\_at S67070 3023 heat shock 27kD protein 2 3.12 up 0.01688<BR> S78187\_at S78187 3036 cell division cycle 25B 4.83 up 0.00547<BR> rc\_T03438\_s\_at T03438 3043 EST 3.79 up 0.02042<BR> rc\_T03580\_f\_at T03580 3046 pyruvate kinase, muscle 5.57 up 0.01344<BR> rc\_T03749\_at T03749 3048 KIAA1089 protein 4.23 up 0.00776<BR> rc\_T10316\_s\_at T10316 3052 EST 3.2 up 0.04794<BR> rc\_T10698\_s\_at T10698 3054 EST 3.86 up 0.00195<BR> rc\_T15852\_f\_at T15852 3062 EST 5.21 up 0.00642 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_T16206\_s\_at T16206 3065 EST 4.29 up 0.00868<BR> rc\_T16226\_at T16226 3066 EST 7.23 up 0.00119<BR> rc\_T16550\_at T16550 3072 vacuolar protein sorting 45B (yeast homolog) 5.88 up 0.00004<BR> rc\_T16652\_s\_at T16652 3073 BCS1 (yeast homolog)-like 3.63 up 0.00434<BR> rc\_T16983\_s\_at T16983 3074 cleavage and polyadenylation specific factor 4, 30kD 4.23 up 0.0106<BR> rc\_T17066\_s\_at T17066 3075 SET domain, bifurcated, 1 5.14 up 0.00073<BR> rc\_T17339\_f\_at T17339 3076 EST 3.29 up 0.00669<BR> rc\_T17353\_s\_at T17353 3077 EST 3.52 up 0.02085<BR> rc\_TV2326\_s\_at T23426 3079 EST 3.51 up 0.00674<BR> rc\_T23465\_at T23465 3081 EST 3.64 up 0.00265<BR> rc\_T23516\_f\_at T23516 3083 3-phosphoglycerate dehydrogenase 3.39 up 0.00551<BR> rc\_T24068\_s\_at T24068 3088 EST 8.65 up 0.00118<BR> rc\_T26471\_at T26471 3094 EST 3.76 up 0.0165<BR> X-ray repair complementing defective repair in Chinese<BR> rc\_T26646\_f\_at T26646 3097 hamster cells 1 3.49 up 0.02482<BR> rc\_T30214\_at T30214 3099 EST 4.46 up 0.03654<BR> rc\_T33489\_s\_at T33489 3105 EST 4.6 up 0.00285<BR> rc\_T33508\_s\_at T33508 3106 phosphatidylinositol-4-phosphate 5-kinase, type II, beta 4.96 up 0.00064<BR> rc\_T33619\_s\_at T33619 3107 EST 3.36 up 0.01283<BR> rc\_T33625\_at T33625 3108 EST 3.36 up 0.04096<BR> rc\_T33859\_at T33859 3109 KIAA0365 gene product 3.9 up 0.0019<BR> potassium voltage-gated channel, shaker-related<BR> T34377\_at T34377 3111 subfamily, beta member 2 4.55 up



0.00041<BR> rc\_T40439\_s\_at T40439 3115 small nuclear ribonucleoprotein polypeptide B" 3.06 up  
0.02842<BR> rc\_T41078\_at T41078 3121 bromodomain adjacent to zinc finger domain, 2B 3.08 up  
0.03426<BR> rc\_T47032\_s\_at T47032 3124 partner of RAC1 (arfaptin 2) 6.09 up 0.00019<BR>  
rc\_T47325\_s\_at T47325 3125 EST 5.6 up 0.02923<BR> ceroid-lipofuscinosis, neuronal 3, juvenile  
(Batten,<BR> rc\_T47969\_s\_at T47969 3128 Spielmeier-Vogt disease) 3.19 up 0.02283<BR>  
rc\_T51972\_at T51972 3140 EST 3.44 up 0.00406 Table 7B. Down regulated in hepatocellular  
carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold  
Change Direction Pvalue<BR> cytochrome P450, subfamily XIA (cholesterol side chain<BR>  
rc\_T53590\_s\_at T53590 3144 cleavage) 5.09 up 0.00002<BR> rc\_T55196\_at T55196 3147 EST 4.24  
up 0.00046<BR> rc\_T58607\_at T58607 3155 EST 6.83 up 0.03711<BR> rc\_T59668\_s\_at T59668  
3160 lysyl oxidase 3.5 up 0.00083<BR> rc\_T62521\_at T62521 3168 EST 4.1 up 0.00392<BR>  
rc\_T62918\_at T62918 3169 EST 5.25 up 0.00687<BR> rc\_T65957\_f\_at T65957 3176 ribosomal  
protein S3A 3.94 up 0.04187<BR> rc\_T66935\_at T66935 3179 EST 3.01 up 0.00123<BR>  
rc\_T67053\_f\_at T67053 3180 EST 5 up 0.01846<BR> rc\_T77733\_s\_at T77733 3219 tubulin, gamma 1  
4 up 0.00526<BR> rc\_T78922\_s\_at T78922 3222 stem cell growth factor; lymphocyte secreted C-type  
3.89 up 0.00604<BR> rc\_T79477\_s\_at T79477 3223 death-associated protein 6 4.4 up 0.00074<BR>  
rc\_T831393\_s\_at T831393 3228 HMT1 (hnRNP methyltransferase, C. cerevisiae)-like 1 3.32 up  
0.0023<BR> rc\_T88814\_at T88814 3242 EST 4.87 up 0.00001<BR> rc\_T89703\_at T89703 3244 EST  
5.27 up 0.00019<BR> rc\_T90190\_s\_at T90190 3247 H1 histone family, member 2 4.88 up  
0.00555<BR> rc\_T94452\_at T94452 3257 EST 3.23 up 0.02245<BR> rc\_T95057\_f\_at T95057 3259  
EST 6.46 up 0.00613<BR> rc\_T97679\_at T97679 3266 EST 3.32 up 0.01566<BR> rc\_T99312\_at  
T99312 3270 EST 3.22 up 0.00084<BR> U18018\_at U18018 3317 ets variant gene 4 (E1A enhancer-  
binding protein, E1AF) 3.9 up 0.0403<BR> U18321\_at U18321 3318 death associated protein 3 3.14 up  
0.00833<BR> proteasome (prosome, macropain) 26S subunit, non-<BR> U24704\_at U24704 3332  
ATPase, 4 3.45 up 0.00037<BR> cyclin-dependent kinase inhibitor 2A melanoma, p16,<BR>  
U26727\_at U26727 3337 inhibits CDK4) 3.53 up 0.02913<BR> U30825\_at U30825 3343 splicing  
factor, arginine/serine-rich 9 3.07 up 0.01928<BR> U45285\_at U45285 3364 T-cell, immune regulator  
1 5.75 up 0.00006<BR> U47025\_s\_at U47025 3368 phosphorylase, glycogen; brain 4.47 up 0.00037  
Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID  
Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> siaH binding protein 1; FBP  
interacting repressor;<BR> pyrimidine tract binding splicing factor; Ro<BR> U51586\_at U51586 3386  
ribonucleoprotein-binding protein 1 3.65 up 0.00403<BR> gamma-glutamyl hydrolase  
(conjugase,<BR> U55206\_at U55206 3392 folylpolyglutaminyl hydrolase) 3.34 up 0.00315<BR>  
U59321\_at U59321 3398 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 3.12 up 0.02469<BR>  
U62392\_at U62392 3403 zinc finger protein 193 3.56 up 0.0407<BR> U66661\_at U66661 3406  
gamma-aminobutyric acid (GABA) A receptor, epsilon 3.55 up 0.0045<BR> U68142\_at U68142 3411  
RAB2, member RAS oncogene family-like 3.02 up 0.0296<BR> SHC (Src homology 2 domain-  
containing) transforming<BR> U73377\_at U73377 3417 protein 1 4.64 up 0.00081<BR> U73379\_at  
U73379 3418 ubiquitin carrier protein E2-C 3.32 up 0.00808<BR> U75285\_rna1\_at U75285 3422  
apoptosis inhibitor 4 (survivin) 5.32 up 0.01127<BR> U85625\_at U85625 3448 ribonuclease 6  
precursor 4 up 0.01664<BR> U90426\_at U90426 3453 nuclear RNA helicase, DECD variant of DEAD  
box family 3.24 up 0.00035<BR> U90551\_at U90551 3457 H2A histone family, member L 3.54 up  
0.01523<BR> U90904\_at U90904 3458 EST 3.02 up 0.00381<BR> U91930\_at U91930 3460 adaptor-  
related protein complex 3, delta 1 subunit 3.68 up 0.00009<BR> rc\_W02041\_at W02041 3466 EST  
5.34 up 0.00027<BR> rc\_W02695\_at W02695 3437 EST 3.1 up 0.04745<BR> rc\_W04507\_s\_at  
W04507 3469 prefoldin 4 3.02 up 0.04091<BR> rc\_W04550\_at W04550 3470 EST 4.01 up  
0.00349<BR> rc\_W15495\_at W15495 3474 chromosome 21 open reading frame 5 3.09 up  
0.00491<BR> W26716\_at W26716 3482 non-histone chromosome protein 2 (S. cerevisiae)-like 1 5.47  
up 0.00146<BR> W28362\_at W28362 3488 KIAA0974 protein 4.38 up 0.00322<BR> W28366\_at  
W28366 3489 EST 3.21 up 0.01007<BR> rc\_W31906\_at W31906 3497 secretogogin 6.62 up  
0.00926<BR> rc\_W42627\_f\_at W42627 3511 EST 4.37 up 0.00021<BR> rc\_W42674\_at W42674

3512 EST 3.07 up 0.0261<BR> rc\_W42778\_at W42778 3513 EST 3.27 up 0.02411<BR> rc\_W42788\_at W42788 3514 deoxynucleotidyltransferase, terminal 3.24 up 0.02261 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> rc\_W42957\_at W42957 3516 calmodulin 2 (phosphorylase kinase, delta) 5.79 up 0.03669<BR> rc\_W44557\_at W44557 3518 chromosome 1 open reading frame 4.1 up 0.00433<BR> rc\_W45320\_f\_at W45320 3523 KRAB-associated protein 1 10.05 up 0.00002<BR> rc\_W46286\_s\_at W46286 3526 EST 3.68 up 0.00311<BR> rc\_W46634\_at W46634 3530 EST 5.03 up 0.02152<BR> rc\_W46810\_s\_at W46810 3531 HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2 3.17 up 0.03434<BR> rc\_W46846\_at W46846 3532 EST 5.11 up 0.00025<BR> rc\_W46947\_at W46947 3533 EST 3.42 up 0.04665<BR> rc\_W47206\_at W47206 3535 EST 3.23 up 0.01931<BR> W49743\_at W49743 3540 EST 3.11 up 0.01121<BR> rc\_W49791\_at W49791 3541 plasminogen activator, tissue 3.58 up 0.02438<BR> rc\_W56642\_at W56642 3547 EST 3.15 up 0.00654<BR> rc\_W57931\_at W57931 3549 EST 3.01 up 0.02661<BR> rc\_W58081\_a tW58081 3550 neuroendocrine-specific protein C like (foocen) 3.05 up 0.03767<BR> W58247\_s\_at W58247 3551 kinesin family member 4 3.08 up 0.00048<BR> DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y<BR> rc\_W60097\_at W60097 3556 chromosome 4.82 up 0.04903<BR> rc\_W60486\_at W60486 3558 EST 4.27 up 0.0046<BR> rc\_W63608\_at W63608 3564 EST 3.33 up 0.02443<BR> W69302\_at W69302 3573 EST 4.37 up 0.00165<BR> rc\_W69468\_at W69468 3574 EST 3.25 up 0.00055<BR> rc\_W70336\_at W70336 3579 EST 4.46 up 0.00023<BR> rc\_W72187\_at W72187 3582 EST 3.09 up 0.00134<BR> rc\_W72276\_at W72276 3583 EST 3.56 up 0.0476<BR> rc\_W73038\_at W73038 3588 EST 4.83 up 0.00902<BR> rc\_W74536\_s\_at W74536 3598 advanced glycosylation end product-specific receptor 3.07 up 0.00251<BR> rc\_W78057\_at W78057 3600 EST 5.53 up 0.01231<BR> rc\_W79421\_at W79421 3603 EST 3.57 up 0.00895<BR> rc\_W79773\_at W79773 3605 EST 4.89 up 0.00034<BR> rc\_W80730\_at W80730 3607 EST 3.35 up 0.01526<BR> rc\_W80763\_at W80763 3608 EST 4.98 up 0.01026 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein<BR> rc\_W80852\_at W80852 3609 retention recepto 3 6.37 up 0.00005<BR> rc\_W81654\_at W81654 3616 SRY (sex determining region Y)-box 13 6.06 up 0.00127<BR> rc\_W84447\_at W84447 3617 EST 3.34 up 0.00986<BR> rc\_W85875\_at W85875 3620 EST 4.91 up 0.01198<BR> rc\_W86214\_at W86214 3625 EST 4.3 up 0.00194<BR> rc\_W86748\_at W86748 3629 EST 5.09 up 0.01182<BR> rc\_W90146\_f\_at W90146 3644 EST 3.58 up 0.00322<BR> rc\_W92608\_s\_at W92608 3653 BA11-associated protein 3 4.84 up 0.00599<BR> rc\_W94281\_s\_at W94281 3658 integral membrane protein 2C 3.51 up 0.01689<BR> rc\_W94885\_at W94885 3660 EST 6.53 up 0<BR> rc\_W95841\_at W95841 3666 EST 3 up 0.00466<BR> X04347\_s\_at X04347 3680 heterogeneous nuclear ribonucleoprotein A1 3.34 up 0.00123<BR> X05610\_at X05610 3685 collagen, type IV, alpha 2 6.04 up 0.00062<BR> collagen, type III, alpha 1 (Ehlers-Danlos syndrome type<BR> X06700\_s\_at X06700 3688 IV, autosomal dominant) 3.58 up 0.02964<BR> keratin 10 (dpidemiolytic hyperkeratosis; keratosis<BR> X14487\_rna1\_s\_at X14487 3702 palmaris et plantaris) 3.19 up 0.01268<BR> X14850\_at X14850 3706 H2A histone family, member X 3.13 up 0.01523<BR> X17567\_s\_at X17567 3719 small nuclear ribonucleoprotein polypeptides B and B1 3.96 up 0.00317<BR> X53331\_at X53331 3727 matrix Gla protein 3.95 up 0.0151<BR> X54667\_s\_at X54667 3731 cystatin S, cystatin SN 3.51 up 0.00187<BR> X54941\_at X54941 3728 CDC28 protein kinase 1 3.99 up 0.0016<BR> X54942\_at X54942 3733 CD28 protein kinase 2 3.8 up 0.0035<BR> X56494\_at X56494 3738 pyruvate kinase, muscle 3.65 up 0.04795<BR> X57129\_at X57129 3743 H1 histone family, member 2 4.63 up 0.00663<BR> X57809\_s\_at X57809 3746 immunoglobulin lambda locus 3.64 up 0.02655<BR> X62153\_s\_at X62153 3754 minichromosome maintenance deficient (S. cerevisiae) 3 3.44 up 0.00704<BR> X62534\_s\_at X62534 3755 high-mobility group (nonhistone chromosomal) protein 2 3.39 up 0.0186<BR> X64364\_at X64364 3764 basigin 3.57 up 0.00902<BR> X66899\_at X66899 3772 Ewing sarcoma breakpoint region 1 3.41 up 0.03777 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue<BR> transmembrane protein (63kD),

endoplasmic<BR> X69910\_at X69910 3787 reticulum/Golgi intermediate compartment 3.35 up  
 0.00898<BR> X74801\_at X74801 3791 chaperonin containing TCP1, subunit 3 (gamma) 3.86 up  
 0.00453<BR> X79563\_at X79563 3804 heterogeneous nuclear ribonucleoprotein A1 3.06 up  
 0.00449<BR> X83425\_at X83425 3812 Lutheran blood group (Auburger b antigen included) 3.66 up  
 0.02661<BR> X87212\_at X87212 3816 cathepsin C 3.45 up 0.02486<BR> DNA segment on  
 chromosome X (unique) 9879<BR> X92896\_at X92896 3829 expressed sequence 3.1 up 0.0405<BR>  
 X99920\_at X99920 3843 S100 calcium-binding protein A13 4.66 up 0.00113<BR> Y00705\_at Y00705  
 3850 serine protease inhibitor, Kazal type 1 28.88 up 0.00003<BR> Y00764\_at Y00764 3851  
 ubiquinol-cytochrome c reductase hinge protein 3.04 up 0.01294<BR> Y08302\_at Y08302 3852 dual  
 specificity phosphatase 9 3.48 up 0.00787<BR> Y08999\_at Y08999 3855 actin related protein 2/3  
 complex, subunit 1A (41 kD) 3.13 up 0.02376<BR> eukaryotic translation elongation factor 1 delta  
 (guanine<BR> Z21507\_at Z21507 3867 nucleotide exchange protein) 3.57 up 0.01898<BR>  
 Z23090\_at Z23090 3868 heat shock 27kD protein 1 3.69 up 0.00628<BR> Z24727\_at Z24727 3871  
 tropomyosin 1 (alpha) 3.64 up 0.00388<BR> Z37987\_s\_at 3797 3882 glypican 3 10.66 up  
 0.02304<BR> rc\_Z38299\_at Z38299 3887 EST 3.71 up 0.0036<BR> rc\_Z38431\_at Z38431 3889 EST  
 3.09 up 0.0083<BR> rc\_Z38444\_at Z38444 3891 KIAA0923 protein 3.38 up 0.02918<BR>  
 rc\_Z38462\_at Z38462 3982 KIAA0938 PROTEIN 4.69 UP 0.0142<BR> rc\_Z38904\_at Z38904 3896 EST  
 3.02 up 0.00814<BR> rc\_Z389191\_at Z389191 3901 EST 3.47 up 0.00756<BR> rc\_Z39200\_at Z39200  
 3902 EST 4.07 up 0.00075<BR> rc\_Z39379\_at Z39379 3903 EST 3.77 up 0.00513<BR> rc\_Z39429\_at  
 Z39429 3906 EST 3.58 up 0.00416<BR> rc\_Z39682\_s\_at Z39682 3911 KIAA0954 protein 6.96 up  
 0.01966<BR> rc\_Z40006\_at Z40006 3917 EST 3.54 up 0.00156<BR> rc\_Z40883\_r\_at Z40883 3924  
 EST 3.26 up 0.01863<BR> rc\_Z41349\_at Z41349 3931 EST 3.45 up 0.01503 Table 7B. Down  
 regulated in hepatocellular carcinoma versus normal sample set 2.<BR> <P>Affy ID Genbank Seq ID  
 Known Gene Name Fold Change Direction Pvalue<BR> succinate dehydrogenase complex, subunit  
 A,<BR> rc\_Z41747\_at Z41747 3936 flavoprotein (Fp) 3.04 up 0.01336<BR> Z47727\_at Z47727 3940  
 polymerase (RNA) II (DNA directed) polypeptide K 3.28 up 0.00317<BR> Z74615\_at Z74615 3949  
 collagen, type I, alpha 1 5.47 up 0.00283<BR> Z74616\_s\_at Z74616 3950 collagen, type I, alpha 2 5.95  
 up 0.02212 Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal  
 sample set 2.<BR> fold hcc hcc hcc<BR> change sample sample sample normal normal normal<BR> in  
 hcc set 2: set 2: set 2: set 2: set 2: set 2:<BR> Affy ID Genbank Seq ID Known Gene Name set 2 p  
 value Mean Median Std Dev Mean Median Std Dev<BR> DEK oncogene (DNA<BR> AA093497\_s\_at  
 AA093497 199 binding) &num;N/A &num;N/A 180.58 107.64 165.71 52.11 48.84 26.51<BR>  
 AA248283\_at AA248283 534 EST &num;N/A &num;N/A 67.18 45.86 55.18 21.63 18.96 11.71<BR>  
 AA291456\_s\_at AA291456 700 EST &num;N/A &num;N/A 828.34 830.24 196.63 671.21 509.58  
 629.13<BR> GAS2-related on<BR> AA400643\_s\_at AA400643 817 chromosome 22 4.04 0.03751  
 118.72 123.18 137.15 -43.6 -33.96 60.39<BR> AA420179\_at AA420179 930 EST &num;N/A  
 &num;N/A 37.17 34.26 18.5 15.27 16.75 15.28<BR> Notch (Drosophila) homolog<BR>  
 AA428172\_f\_at AA428172 986 3 9.68 0.00195 335.57 374.9 231.52 -9.64 -15.61 56.16<BR>  
 AA464043\_s\_at AA464043 1255 EST 3.99 0.00056 116.97 115.99 53.49 14.27 10.06 25.86<BR>  
 H19562\_at H19562 1896 PTD010 protein &num;N/A #N/A 522.13 432.65 256.94 393.61 326.53  
 182.71<BR> L08044\_s\_at L08044 2149 trefoil factor 3 (intestinal) &num;N/A &num;N/A 214.6  
 108.17 238.79 107.82 58.55 184.16<BR> L29218\_s\_at L29218 2190 CDC-like kinase 2 6.51 0.00019  
 219.64 237.35 104.29 6.53 -10.03 59.8<BR> L37747\_s\_at L37747 2206 lamin B1 &num;N/A  
 &num;N/A 43.42 28.65 37.33 5.97 5.1 7.57<BR> N34257\_at N34257 2495 EST &num;N/A  
 &num;N/A 20.76 21.48 19.54 -1.84 -2.74 8.53<BR> R50692\_at R50692 2888 KIAA0476 gene  
 product &num;N/A &num;N/A 197.89 187.87 101.08 148.53 151.12 63.03<BR> R60368\_at R60368  
 2917 EST &num;N/A &num;N/A 29.68 28.93 31.9 -28.29 -26.44 41.68<BR> R66475\_at R66475 2938  
 EST &num;N/A &num;N/A 45.68 32.34 34.37 7.64 8.26 6.3<BR> potassium voltage-gated<BR>  
 channel, shaker-related<BR> T34377\_at T34377 3111 subfamily, beta member 2 4.55 0.00041 113.59  
 120.58 51.65 6.87 11.17 25.69<BR> DEAD/H (Asp-Glu-Ala-<BR> Asp/His) box polypeptide 11<BR>  
 (S.cerevisiae CHL1-like<BR> V75968\_s\_at U75968 3423 helicase) &num;N/A &num;N/A 187.33

200.16 90.35 115.5 102.24 77.72<BR> W21426\_at W21426 381 KIAA0806 gene product &num;N/A  
&num;N/A 63.36 64.93 20.23 45.59 40.39 19.89<BR> W28696\_i\_at W28696 3491 EST &num;N/A  
&num;N/A 14.7 20.64 17.12 4.28 4.33 2.47 Table 8A. Genes and ESTs expressed only in hepatocellular  
carcinoma versus normal sample set 2.<BR> fold hcc hcc hcc<BR> change sample sample sample  
normal normal normal<BR> in hcc set 2: set 2: set 2: set 2: set 2: set 2:<BR> Affy ID Genbank Seq ID  
Known Gene Name set 2 p value Mean Median Std Dev Mean Median Std Dev<BR> H1 histone  
family, member<BR> X57129\_at X57129 3743 2 4.63 0.00663 137.13 137.75 87.31 8.38 5.39  
28.3<BR> rc\_AA024658\_at AA024658 47 ribosomal protein S19 7.55 0.00592 278.11 120.83 373.3  
7.62 5.03 10.68<BR> rc\_AA029288\_at AA029288 65 EST 3.36 0.04908 134.53 56.15 209.69 4.09 3.35  
8.39<BR> rc\_AA037828\_at AA037828 88 KIAA0614 protein &num;N/A &num;N/A 53.61 46.86  
41.68 13.32 10.65 11.96<BR> rc\_AA040465\_at AA040465 95 EST 3.63 0.01806 229.8 210.67 180.94  
47.15 45.53 5.48<BR> rc\_AA053660\_at AA053660 128 EST &num;N/A &num;N/A 543.66 223.47  
685.44 95.24 79.97 42.99<BR> cAMP responsive element<BR> rc\_AA136332\_at AA136332 299  
binding protein 3 (human) &num;N/A &num;N/A 49.04 33.07 31.07 -18.27 -20.23 13.05<BR>  
rc\_AA149530\_at AA149530 324 interferon regulatory factor 3 &num;N/A &num;N/A 32.94 23.12  
34.23 4.21 5.38 8.53<BR> rc\_AA149586\_at AA149586 325 EST &num;N/A &num;N/A 24.99 26.6  
34.37 5.26 9.11 23.41<BR> rc\_AA206023\_at AA206023 427 EST &num;N/A &num;N/A 154.13  
170.36 85.33 108.57 111.76 58.39<BR> N-ethylmaleimide-sensitive<BR> rc\_aa234530\_s\_at  
AA234530 484 factor &num;N/A &num;N/A 143.67 135.48 82.59 51.33 42.9 35.02<BR>  
rc\_AA251909\_at AA251909 549 EST 3.59 0.01129 92.19 79.34 72.73 8.88 11.22 8.27<BR>  
rc\_AA262030\_at AA262030 605 EST &num;N/A &num;N/A 119.75 89.66 103.84 31.51 32.91  
14.46<BR> ribonuclease HI, large<BR> rc\_AA262477\_at AA262477 608 subunit 4.57 0.00724 242.42  
199.5 182.26 44.51 36.87 22.37<BR> rc\_AA283759\_at AA283759 671 EST &num;N/A &num;N/A  
91.82 76.73 42.28 46.87 45.86 21.54<BR> rc\_AA291644\_at AA291644 701 EST 3.28 0.00033 11473  
117.29 44.59 32.77 30.24 21.1<BR> rc\_AA338760\_at AA338760 744 EST 3.96 0.01307 129.77 130.26  
87.27 14.91 21.91 26.96<BR> rc\_RC398205\_at AA398205 789 EST 4.22 0.00059 125.4 107.84 63.85  
15.01 7.37 26.26<BR> tumor suppressor deleted in<BR> rc\_AA401965\_at AA401965 833 oral cancer-  
related 1 7.58 0.00089 932.74 924.02 593.69 120.58 93.29 109.41<BR> rc\_AA402272\_at AA402272  
837 EST 3.73 0.02336 348.91 340 230.15 99.7 92.28 80.27<BR> rc\_AA404597\_at AA404597 854 EST  
&num;N/A &num;N/A 609.98 525.02 371.31 379.26 336.33 167.43<BR> rc\_AA417030\_at AA417030  
914 EST 7.35 0.00555 200.3 168.21 135.63 6.42 7.5 7.77 Table 8A. Genes and ESTs expressed only in  
hepatocellular carcinoma versus normal sample set 2.<BR> fold hcc hcc hcc<BR> change sample  
sample sample normal normal normal<BR>